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SEQUENCE LISTING

A12
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<120> CLASP-7 Transmembrane Protein

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<140> US 09/736,968

<141> 2000-12-13

<150> US 60/160,860

<151> 1999-10-21

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<151> 2000-02-14

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RECEIVED

OCT 17 2001

TECH CENTER 1600/2900

<170> PatentIn Ver. 2.1

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gcc cag gtg ttt tta gca gag atc ccg gaa gac ccc aag ctc ttc cgg Ala Gln Val Phe Leu Ala Glu Ile Pro Glu Asp Pro Lys Leu Phe Arg 1950 1955 1960 1965	5907
cat cac aac aaa ttg cgg ctc tgc ttc aag gac ttc tgc aag aaa tgt His His Asn Lys Leu Arg Leu Cys Phe Lys Asp Phe Cys Lys Lys Cys 1970 1975 1980	5955
gag gat gcg ctg cgg aaa aat aag gcc ctg att ggg ccg gac cag aag Glu Asp Ala Leu Arg Lys Asn Lys Ala Leu Ile Gly Pro Asp Gln Lys 1985 1990 1995	6003
gag tac cac cgt gag ctg gag cgc aac tac tgc cgc ctg cgg gag gct Glu Tyr His Arg Glu Leu Glu Arg Asn Tyr Cys Arg Leu Arg Glu Ala 2000 2005 2010	6051
ctg cag ccc ctg ctt acc cag cgc ctg ccc cag ctg atg gca ccc acc Leu Gln Pro Leu Leu Thr Gln Arg Leu Pro Gln Leu Met Ala Pro Thr 2015 2020 2025	6099
cca ccc ggc ctc agg aac tcc ttg aac aga gca agt ttc cga aag gca Pro Pro Gly Leu Arg Asn Ser Leu Asn Arg Ala Ser Phe Arg Lys Ala 2030 2035 2040 2045	6147
gac ctc tga gccacaagg accaaagctg tacctagagg aaccagcacc Asp Leu	6196
cgggcctcag ctgtctgtgc tgcgagggga gtctgccctg gtgcccactg ggctgtgggg	6256
tgaccacact gtacttgggg ctgggccctc tgcccctgtg tccccatctg tgtgcactga	6316
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<210> 2
 <211> 2047
 <212> PRT
 <213> Homo sapiens
 <223> full length human CLASP-7

<400> 2

Met	Ala	Ala	Ser	Glu	Arg	Arg	Ala	Phe	Ala	His	Lys	Ile	Asn	Arg	Thr	1	5	10	15
Val	Ala	Ala	Glu	Val	Arg	Lys	Gln	Val	Ser	Arg	Glu	Arg	Ser	Gly	Ser	20	25	30	
Pro	His	Ser	Ser	Arg	Arg	Cys	Ser	Ser	Ser	Leu	Gly	Val	Pro	Leu	Thr	35	40	45	
Glu	Val	Val	Glu	Pro	Leu	Asp	Phe	Glu	Asp	Val	Leu	Leu	Ser	Arg	Pro	50	55	60	
Pro	Asp	Ala	Glu	Pro	Gly	Pro	Leu	Arg	Asp	Leu	Val	Glu	Phe	Pro	Ala	65	70	75	80
Asp	Asp	Leu	Glu	Leu	Leu	Leu	Gln	Pro	Arg	Glu	Cys	Arg	Thr	Thr	Glu	85	90	95	
Pro	Gly	Ile	Pro	Lys	Asp	Glu	Lys	Leu	Asp	Ala	Gln	Val	Arg	Ala	Ala	100	105	110	
Val	Glu	Met	Tyr	Ile	Glu	Asp	Trp	Val	Ile	Val	His	Arg	Arg	Tyr	Gln	115	120	125	
Tyr	Leu	Ser	Ala	Ala	Tyr	Ser	Pro	Val	Thr	Thr	Asp	Thr	Gln	Arg	Glu	130	135	140	
Arg	Gln	Lys	Gly	Leu	Pro	Arg	Gln	Val	Phe	Glu	Gln	Asp	Ala	Ser	Gly	145	150	155	160
Asp	Glu	Arg	Ser	Gly	Pro	Glu	Asp	Ser	Asn	Asp	Ser	Arg	Arg	Gly	Ser	165	170	175	
Gly	Ser	Pro	Glu	Asp	Thr	Pro	Arg	Ser	Ser	Gly	Ala	Ser	Ser	Ile	Phe	180	185	190	
Asp	Leu	Arg	Asn	Leu	Ala	Ala	Asp	Ser	Leu	Leu	Pro	Ser	Leu	Leu	Glu	195	200	205	
Arg	Ala	Ala	Pro	Glu	Asp	Val	Asp	Arg	Arg	Asn	Glu	Thr	Leu	Arg	Arg	210	215	220	
Gln	His	Arg	Pro	Pro	Ala	Leu	Leu	Thr	Leu	Tyr	Pro	Ala	Pro	Asp	Glu	225	230	235	240
Asp	Glu	Ala	Val	Glu	Arg	Cys	Ser	Arg	Pro	Glu	Pro	Pro	Arg	Glu	His	245	250	255	
Phe	Gly	Gln	Arg	Ile	Leu	Val	Lys	Cys	Leu	Ser	Leu	Lys	Phe	Glu	Ile	260	265	270	
Glu	Ile	Glu	Pro	Ile	Phe	Gly	Ile	Leu	Ala	Leu	Tyr	Asp	Val	Arg	Glu	275	280	285	

Lys Lys Lys Ile Ser Glu Asn Phe Tyr Phe Asp Leu Asn Ser Asp Ser
 290 295 300
 Met Lys Gly Leu Leu Arg Ala His Gly Thr His Pro Ala Ile Ser Thr
 305 310 315 320
 Leu Ala Arg Ser Ala Ile Phe Ser Val Thr Tyr Pro Ser Pro Asp Ile
 325 330 335
 Phe Leu Val Ile Lys Leu Glu Lys Val Leu Gln Gln Gly Asp Ile Ser
 340 345 350
 Glu Cys Cys Glu Pro Tyr Met Val Leu Lys Glu Val Asp Thr Ala Lys
 355 360 365
 Asn Lys Glu Lys Leu Glu Lys Leu Arg Leu Ala Ala Glu Gln Phe Cys
 370 375 380
 Thr Arg Leu Gly Arg Tyr Arg Met Pro Phe Ala Trp Thr Ala Val His
 385 390 395 400
 Leu Ala Asn Ile Val Ser Ser Ala Gly Gln Leu Asp Arg Asp Ser Asp
 405 410 415
 Ser Glu Gly Glu Arg Arg Pro Ala Trp Thr Asp Arg Arg Arg Arg Gly
 420 425 430
 Pro Gln Asp Arg Ala Ser Ser Gly Asp Asp Ala Cys Ser Phe Ser Gly
 435 440 445
 Phe Arg Pro Ala Thr Leu Thr Val Thr Asn Phe Phe Lys Gln Glu Ala
 450 455 460
 Glu Arg Leu Ser Asp Glu Asp Leu Phe Lys Phe Leu Ala Asp Met Arg
 465 470 475 480
 Arg Pro Ser Ser Leu Leu Arg Arg Leu Arg Pro Val Thr Ala Gln Leu
 485 490 495
 Lys Ile Asp Ile Ser Pro Ala Pro Glu Asn Pro His Phe Cys Leu Ser
 500 505 510
 Pro Glu Leu Leu His Ile Lys Pro Tyr Pro Asp Pro Arg Gly Arg Pro
 515 520 525
 Thr Lys Glu Ile Leu Glu Phe Pro Ala Arg Glu Val Tyr Ala Pro His
 530 535 540
 Thr Ser Tyr Arg Asn Leu Leu Tyr Val Tyr Pro His Ser Leu Asn Phe
 545 550 555 560
 Ser Ser Arg Gln Gly Ser Val Arg Asn Leu Ala Val Arg Val Gln Tyr
 565 570 575
 Met Thr Gly Glu Asp Pro Ser Gln Ala Leu Pro Val Ile Phe Gly Lys
 580 585 590
 Ser Ser Cys Ser Glu Phe Thr Arg Glu Ala Phe Thr Pro Val Val Tyr
 595 600 605

His	Asn	Lys	Ser	Pro	Glu	Phe	Tyr	Glu	Glu	Phe	Lys	Leu	His	Leu	Pro	610	615	620
Ala	Cys	Val	Thr	Glu	Asn	His	His	Leu	Leu	Phe	Thr	Phe	Tyr	His	Val	625	630	635
Ser	Cys	Gln	Pro	Arg	Pro	Gly	Thr	Ala	Leu	Glu	Thr	Pro	Val	Gly	Phe	645	650	655
Thr	Trp	Ile	Pro	Leu	Leu	Gln	His	Gly	Arg	Leu	Arg	Thr	Gly	Pro	Phe	660	665	670
Cys	Leu	Pro	Val	Ser	Val	Asp	Gln	Pro	Pro	Pro	Ser	Tyr	Ser	Val	Leu	675	680	685
Thr	Pro	Asp	Val	Ala	Leu	Pro	Gly	Met	Arg	Trp	Val	Asp	Gly	His	Lys	690	695	700
Gly	Val	Phe	Ser	Val	Glu	Leu	Thr	Ala	Val	Ser	Ser	Val	His	Pro	Gln	705	710	715
Asp	Pro	Tyr	Leu	Asp	Lys	Phe	Phe	Thr	Leu	Val	His	Val	Leu	Glu	Glu	725	730	735
Gly	Ala	Phe	Pro	Phe	Arg	Leu	Lys	Asp	Thr	Val	Leu	Ser	Glu	Gly	Asn	740	745	750
Val	Glu	Gln	Glu	Leu	Arg	Ala	Ser	Leu	Ala	Ala	Leu	Arg	Leu	Ala	Ser	755	760	765
Pro	Glu	Pro	Leu	Val	Ala	Phe	Ser	His	His	Val	Leu	Asp	Lys	Leu	Val	770	775	780
Arg	Leu	Val	Ile	Arg	Pro	Pro	Ile	Ile	Ser	Gly	Gln	Ile	Val	Asn	Leu	785	790	795
Gly	Arg	Gly	Ala	Phe	Glu	Ala	Met	Ala	His	Val	Val	Ser	Leu	Val	His	805	810	815
Arg	Ser	Leu	Glu	Ala	Ala	Gln	Asp	Ala	Arg	Gly	His	Cys	Pro	Gln	Leu	820	825	830
Ala	Ala	Tyr	Val	His	Tyr	Ala	Phe	Arg	Leu	Pro	Gly	Thr	Glu	Pro	Ser	835	840	845
Leu	Pro	Asp	Gly	Ala	Pro	Pro	Val	Thr	Val	Gln	Ala	Ala	Thr	Leu	Ala	850	855	860
Arg	Gly	Ser	Gly	Arg	Pro	Ala	Ser	Leu	Tyr	Leu	Ala	Arg	Ser	Lys	Ser	865	870	875
Ile	Ser	Ser	Ser	Asn	Pro	Asp	Leu	Ala	Val	Ala	Pro	Gly	Ser	Val	Asp	885	890	895
Asp	Glu	Val	Ser	Arg	Ile	Leu	Ala	Ser	Lys	Leu	Leu	His	Glu	Glu	Leu	900	905	910
Ala	Leu	Gln	Trp	Val	Val	Ser	Ser	Ser	Ala	Val	Arg	Glu	Ala	Ile	Leu	915	920	925

Gln His Ala Trp Phe Phe Phe Gln Leu Met Val Lys Ser Met Ala Leu
 930 935 940
 His Leu Leu Leu Gly Gln Arg Leu Asp Thr Pro Arg Lys Leu Arg Phe
 945 950 955 960
 Pro Gly Arg Phe Leu Asp Asp Ile Thr Ala Leu Val Gly Ser Val Gly
 965 970 975
 Leu Glu Val Ile Thr Arg Val His Lys Asp Val Glu Leu Ala Glu His
 980 985 990
 Leu Asn Ala Ser Leu Ala Phe Phe Leu Ser Asp Leu Leu Ser Leu Val
 995 1000 1005
 Asp Arg Gly Phe Val Phe Ser Leu Val Arg Ala His Tyr Lys Gln Val
 1010 1015 1020
 Ala Thr Arg Leu Gln Ser Ser Pro Asn Pro Ala Ala Leu Leu Thr Leu
 1025 1030 1035 1040
 Arg Met Glu Phe Thr Arg Ile Leu Cys Ser His Glu His Tyr Val Thr
 1045 1050 1055
 Leu Asn Leu Pro Cys Cys Pro Leu Ser Pro Pro Ala Ser Pro Ser Pro
 1060 1065 1070
 Ser Val Ser Ser Thr Thr Ser Gln Ser Ser Thr Phe Ser Ser Gln Ala
 1075 1080 1085
 Pro Asp Pro Lys Val Thr Ser Met Phe Glu Leu Ser Gly Pro Phe Arg
 1090 1095 1100
 Gln Gln His Phe Leu Ala Gly Leu Leu Leu Thr Glu Leu Ala Leu Ala
 1105 1110 1115 1120
 Leu Glu Pro Glu Ala Glu Gly Ala Phe Leu Leu His Lys Lys Ala Ile
 1125 1130 1135
 Ser Ala Val His Ser Leu Leu Cys Gly His Asp Thr Asp Pro Arg Tyr
 1140 1145 1150
 Ala Glu Ala Thr Val Lys Ala Arg Val Ala Glu Leu Tyr Leu Pro Leu
 1155 1160 1165
 Leu Ser Ile Ala Arg Asp Thr Leu Pro Arg Leu His Asp Phe Ala Glu
 1170 1175 1180
 Gly Pro Gly Gln Arg Ser Arg Leu Ala Ser Met Leu Asp Ser Asp Thr
 1185 1190 1195 1200
 Glu Gly Glu Gly Asp Ile Ala Gly Thr Ile Asn Pro Ser Val Ala Met
 1205 1210 1215
 Ala Ile Ala Gly Gly Pro Leu Ala Pro Gly Ser Arg Ala Ser Ile Ser
 1220 1225 1230
 Gln Gly Pro Pro Thr Ala Ser Arg Ala Gly Cys Ala Leu Ser Ala Glu
 1235 1240 1245

Ser Ser Arg Thr Leu Leu Ala Cys Val Leu Trp Val Leu Lys Asn Thr
 1250 1255 1260
 Glu Pro Ala Leu Leu Gln Arg Trp Ala Thr Asp Leu Thr Leu Pro Gln
 1265 1270 1275 1280
 Leu Gly Arg Leu Leu Asp Leu Leu Tyr Leu Cys Leu Ala Ala Phe Glu
 1285 1290 1295
 Tyr Lys Gly Lys Lys Ala Phe Glu Arg Ile Asn Ser Leu Thr Phe Lys
 1300 1305 1310
 Lys Ser Leu Asp Met Lys Ala Arg Leu Glu Glu Ala Ile Leu Gly Thr
 1315 1320 1325
 Ile Gly Ala Arg Gln Glu Met Val Arg Arg Ser Arg Glu Arg Ser Pro
 1330 1335 1340
 Phe Gly Asn Pro Glu Asn Val Arg Trp Arg Lys Ser Val Thr His Trp
 1345 1350 1355 1360
 Lys Gln Thr Ser Asp Arg Val Asp Lys Thr Lys Asp Glu Met Glu His
 1365 1370 1375
 Glu Ala Leu Val Glu Gly Asn Leu Ala Thr Glu Ala Ser Leu Val Val
 1380 1385 1390
 Leu Asp Thr Leu Glu Ile Ile Val Gln Thr Val Met Leu Ser Glu Ala
 1395 1400 1405
 Arg Glu Ser Val Leu Gly Ala Val Leu Lys Val Val Leu Tyr Ser Leu
 1410 1415 1420
 Gly Ser Ala Gln Ser Ala Leu Phe Leu Gln His Gly Leu Ala Thr Gln
 1425 1430 1435 1440
 Arg Ala Leu Val Ser Lys Phe Pro Glu Leu Leu Phe Glu Glu Asp Thr
 1445 1450 1455
 Glu Leu Cys Ala Asp Leu Cys Leu Arg Leu Leu Arg His Cys Gly Ser
 1460 1465 1470
 Arg Ile Ser Thr Ile Arg Thr His Ala Ser Ala Ser Leu Tyr Leu Leu
 1475 1480 1485
 Met Arg Gln Asn Phe Glu Ile Gly His Asn Phe Ala Arg Val Lys Met
 1490 1495 1500
 Gln Val Thr Met Ser Leu Ser Ser Leu Val Gly Thr Thr Gln Asn Phe
 1505 1510 1515 1520
 Ser Glu Glu His Leu Arg Arg Ser Leu Lys Thr Ile Leu Thr Tyr Ala
 1525 1530 1535
 Glu Glu Asp Met Gly Leu Arg Asp Ser Thr Phe Ala Glu Gln Val Gln
 1540 1545 1550
 Asp Leu Met Phe Asn Leu His Met Ile Leu Thr Asp Thr Val Lys Met
 1555 1560 1565

Lys Glu His Gln Glu Asp Pro Glu Met Leu Ile Asp Leu Met Tyr Arg
 1570 1575 1580
 Ile Ala Arg Gly Tyr Gln Gly Ser Pro Asp Leu Arg Leu Thr Trp Leu
 1585 1590 1595 1600
 Gln Asn Met Ala Gly Lys His Ala Glu Leu Gly Asn His Ala Glu Ala
 1605 1610 1615
 Ala Gln Cys Met Val His Ala Ala Ala Leu Val Ala Glu Tyr Leu Ala
 1620 1625 1630
 Leu Leu Glu Asp Gln Arg His Leu Pro Val Gly Cys Val Ser Phe Gln
 1635 1640 1645
 Asn Ile Ser Ser Asn Val Leu Glu Glu Ser Ala Ile Ser Asp Asp Ile
 1650 1655 1660
 Leu Ser Pro Asp Glu Glu Gly Phe Cys Ser Gly Lys His Phe Thr Glu
 1665 1670 1675 1680
 Leu Gly Leu Val Gly Leu Leu Glu Gln Ala Ala Gly Tyr Phe Thr Met
 1685 1690 1695
 Gly Gly Leu Tyr Glu Ala Val Asn Glu Val Tyr Lys Asn Leu Ile Pro
 1700 1705 1710
 Ile Leu Glu Ala His Arg Asp Tyr Lys Lys Leu Ala Ala Val His Gly
 1715 1720 1725
 Lys Leu Gln Glu Ala Phe Thr Lys Ile Met His Gln Ser Ser Gly Trp
 1730 1735 1740
 Glu Arg Val Phe Gly Thr Tyr Phe Arg Val Gly Phe Tyr Gly Ala His
 1745 1750 1755 1760
 Phe Gly Asp Leu Asp Glu Gln Glu Phe Val Tyr Lys Glu Pro Ser Ile
 1765 1770 1775
 Thr Lys Leu Ala Glu Ile Ser His Arg Leu Glu Glu Phe Tyr Thr Glu
 1780 1785 1790
 Arg Phe Gly Asp Asp Val Val Glu Ile Ile Lys Asp Ser Tyr Pro Val
 1795 1800 1805
 Asp Lys Ser Lys Leu Asp Ser Gln Lys Ala Tyr Ile Gln Ile Thr Tyr
 1810 1815 1820
 Val Glu Pro Tyr Phe Asp Thr Tyr Glu Leu Lys Asp Arg Val Thr Tyr
 1825 1830 1835 1840
 Phe Asp Arg Asn Tyr Gly Leu Arg Thr Phe Leu Phe Cys Thr Pro Phe
 1845 1850 1855
 Thr Pro Asp Gly Arg Ala His Gly Glu Leu Pro Glu Gln His Lys Arg
 1860 1865 1870
 Lys Thr Leu Leu Ser Thr Asp His Ala Phe Pro Tyr Ile Lys Thr Arg
 1875 1880 1885

Ile Arg Val Cys His Arg Glu Glu Thr Val Leu Thr Pro Val Glu Val
 1890 1895 1900
 Ala Ile Glu Asp Met Gln Lys Lys Thr Arg Glu Leu Ala Phe Ala Thr
 1905 1910 1915 1920
 Glu Gln Asp Pro Pro Asp Ala Lys Met Leu Gln Met Val Leu Gln Gly
 1925 1930 1935
 Ser Val Gly Pro Thr Val Asn Gln Gly Pro Leu Glu Val Ala Gln Val
 1940 1945 1950
 Phe Leu Ala Glu Ile Pro Glu Asp Pro Lys Leu Phe Arg His His Asn
 1955 1960 1965
 Lys Leu Arg Leu Cys Phe Lys Asp Phe Cys Lys Lys Cys Glu Asp Ala
 1970 1975 1980
 Leu Arg Lys Asn Lys Ala Leu Ile Gly Pro Asp Gln Lys Glu Tyr His
 1985 1990 1995 2000
 Arg Glu Leu Glu Arg Asn Tyr Cys Arg Leu Arg Glu Ala Leu Gln Pro
 2005 2010 2015
 Leu Leu Thr Gln Arg Leu Pro Gln Leu Met Ala Pro Thr Pro Pro Gly
 2020 2025 2030
 Leu Arg Asn Ser Leu Asn Arg Ala Ser Phe Arg Lys Ala Asp Leu
 2035 2040 2045

<210> 3
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 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: furin protease
 consensus cleavage sequence

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 Arg Lys Gln Arg
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<210> 4
 <211> 4
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: CLASP-7 homolog
 of furin protease consensus cleavage sequence

<400> 4
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 1

<210> 5
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 (ITAM) 1

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<210> 6
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 <212> PRT
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<220>
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 immunoreceptor tyrosine-based activation motif
 (ITAM) 2

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 <222> (1)..(13)
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 1 5 10

<210> 7
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
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 conserved non-tyrosine containing region from
 motif E

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 <223> Xaa = conservative amino acid substitution, Ile or
 Leu

<220>
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 <223> Xaa = any amino acid

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<220>
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<222> (7)
<223> Xaa = conservative amino acid substitution, Asp,
      Glu or Gln

<220>
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<210> 8
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<213> Artificial Sequence

<220>
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      motif F

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<220>
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<222> (6)
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      Asn

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<221> MOD_RES
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Glu Leu Pro Thr Gln Leu His Glu Lys His His Leu Leu Leu Thr Phe
      20               25               30

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Phe	His	Val	Ser	Cys	Asp	Asn	Ser	Ser	Lys	Gly	Ser	Thr	Lys	Lys	Arg	35	40	45	
Asp	Val	Val	Glu	Thr	Gln	Val	Gly	Tyr	Ser	Trp	Leu	Pro	Leu	Leu	Lys	50	55	60	
Asp	Gly	Arg	Val	Val	Thr	Ser	Glu	Gln	His	Ile	Pro	Val	Ser	Ala	Asn	65	70	75	80
Leu	Pro	Ser	Gly	Tyr	Leu	Gly	Tyr	Gln	Glu	Leu	Gly	Met	Gly	Arg	His	85	90	95	
Tyr	Gly	Pro	Glu	Ile	Lys	Trp	Val	Asp	Gly	Gly	Lys	Pro	Leu	Leu	Lys	100	105	110	
Ile	Ser	Thr	His	Leu	Val	Ser	Thr	Val	Tyr	Thr	Gln	Asp	Gln	His	Leu	115	120	125	
His	Asn	Phe	Phe	Gln	Tyr	Cys	Gln	Lys	Thr	Glu	Ser	Gly	Ala	Gln	Ala	130	135	140	
Leu	Gly	Asn	Glu	Leu	Val	Lys	Tyr	Leu	Lys	Ser	Leu	His	Ala	Met	Glu	145	150	155	160
Gly	His	Val	Met	Ile	Ala	Phe	Leu	Pro	Thr	Ile	Leu	Asn	Gln	Leu	Phe	165	170	175	
Arg	Val	Leu	Thr	Arg	Ala	Thr	Gln	Glu	Glu	Val	Ala	Val	Asn	Val	Thr	180	185	190	
Arg	Val	Ile	Ile	His	Val	Val	Ala	Gln	Cys	His	Glu	Glu	Gly	Leu	Glu	195	200	205	
Ser	His	Leu	Arg	Ser	Tyr	Val	Lys	Tyr	Ala	Tyr	Lys	Ala	Glu	Pro	Tyr	210	215	220	
Val	Ala	Ser	Glu	Tyr	Lys	Thr	Val	His	Glu	Glu	Leu	Thr	Lys	Ser	Met	225	230	235	240
Thr	Thr	Ile	Leu	Lys	Pro	Ser	Ala	Asp	Phe	Leu	Thr	Ser	Asn	Lys	Leu	245	250	255	
Leu	Arg	Tyr	Ser	Trp	Phe	Phe	Phe	Asp	Val	Leu	Ile	Lys	Ser	Met	Ala	260	265	270	
Gln	His	Leu	Ile	Glu	Asn	Ser	Lys	Val	Lys	Leu	Leu	Arg	Asn	Gln	Arg	275	280	285	
Phe	Pro	Ala	Ser	Tyr	His	His	Ala	Ala	Glu	Thr	Val	Val	Asn	Met	Leu	290	295	300	
Met	Pro	His	Ile	Thr	Gln	Lys	Phe	Gly	Asp	Asn	Pro	Glu	Ala	Ser	Lys	305	310	315	320
Asn	Ala	Asn	His	Ser	Leu	Ala	Val	Phe	Ile	Lys	Arg	Cys	Phe	Thr	Phe	325	330	335	
Met	Asp	Arg	Gly	Phe	Val	Phe	Lys	Gln	Ile	Asn	Asn	Tyr	Ile	Ser	Cys	340	345	350	

Phe Ala Pro Gly Asp Pro Lys Thr Leu Phe Glu Tyr Lys Phe Glu Phe
355 360 365
Leu Arg Val Val Cys Asn His Glu His Tyr Ile Pro Leu Asn Leu Pro
370 375 380
Met Pro Phe Gly Lys Gly Arg Ile Gln Arg Tyr Gln Asp Leu Gln Leu
385 390 395 400
Asp Tyr Ser Leu Thr Asp Glu Phe Cys Arg Asn His Phe Leu Val Gly
405 410 415
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420 425 430
Arg Leu Ile Ala Ile Ser Val Leu Lys Asn Leu Leu Ile Lys His Ser
435 440 445
Phe Asp Asp Arg Tyr Ala Ser Arg Ser His Gln Ala Arg Ile Ala Thr
450 455 460
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465 470 475 480
Asn Val Arg Asp Val Ser Pro Phe Pro Val Asn Ala Gly Met Thr Val
485 490 495
Lys Asp Glu Ser Leu Ala Leu Pro Ala Val Asn Pro Leu Val Thr Pro
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Gln Lys Gly Ser Thr Leu Asp Asn Ser Leu His Lys Asp Leu Leu Gly
515 520 525
Ala Ile Ser Gly Ile Ala Ser Pro Tyr Thr Thr Ser Thr Pro Asn Ile
530 535 540
Asn Ser Val Arg Asn Ala Asp Ser Arg Gly Ser Leu Ile Ser Thr Asp
545 550 555 560
Ser Gly Asn Ser Leu Pro Glu Arg Asn Ser Glu Lys Ser Asn Ser Leu
565 570 575
Asp Lys His Gln Gln Ser Ser Thr Leu Gly Asn Ser Val Val Arg Cys
580 585 590
Asp Lys Leu Asp Gln Ser Glu Ile Lys Ser Leu Leu Met Cys Phe Leu
595 600 605
Tyr Ile Leu Lys Ser Met Ser Asp Asp Ala Leu Phe Thr Tyr Trp Asn
610 615 620
Lys Ala Ser Thr Ser Glu Leu Met Asp Phe Phe Thr Ile Ser Glu Val
625 630 635 640
Cys Leu His Gln Phe Gln Tyr Met Gly Lys Arg Tyr Ile Ala Arg Asn
645 650 655
Gln Glu Gly Leu Gly Pro Ile Val His Asp Arg Lys Ser Gln Thr Leu
660 665 670

Pro Val Ser Arg Asn Arg Thr Gly Met Met His Ala Arg Leu Gln Gln
 675 680 685
 Leu Gly Ser Leu Asp Asn Ser Leu Thr Phe Asn His Ser Tyr Gly His
 690 695 700
 Ser Asp Ala Asp Val Leu His Gln Ser Leu Leu Glu Ala Asn Ile Ala
 705 710 715 720
 Thr Glu Val Cys Leu Thr Ala Leu Asp Thr Leu Ser Leu Phe Thr Leu
 725 730 735
 Ala Phe Lys Asn Gln Leu Leu Ala Asp His Gly His Asn Pro Leu Met
 740 745 750
 Lys Lys Val Phe Asp Val Tyr Leu Cys Phe Leu Gln Lys His Gln Ser
 755 760 765
 Glu Thr Ala Leu Lys Asn Val Phe Thr Ala Leu Arg Ser Leu Ile Tyr
 770 775 780
 Lys Phe Pro Ser Thr Phe Tyr Glu Gly Arg Ala Asp Met Cys Ala Ala
 785 790 795 800
 Leu Cys Tyr Glu Ile Leu Lys Cys Cys Asn Ser Lys Leu Ser Ser Ile
 805 810 815
 Arg Thr Glu Ala Ser Gln Leu Leu Tyr Phe Leu Met Arg Asn Asn Phe
 820 825 830
 Asp Tyr Thr Gly Lys Lys Ser Phe Val Arg Thr His Leu Gln Val Ile
 835 840 845
 Ile Ser Val Ser Gln Leu Ile Ala Asp Val Val Gly Ile Gly Glu Thr
 850 855 860
 Arg Phe Gln Gln Ser Leu Ser Ile Ile Asn Asn Cys Ala Asn Ser Asp
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 Arg Leu Ile Lys His Thr Ser Phe Ser Ser Asp Val Lys Asp Leu Thr
 885 890 895
 Lys Arg Ile Arg Thr Val Leu Met Ala Thr Ala Gln Met Lys Glu His
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 Glu Asn Asp Pro Glu Met Leu Val Asp Leu Gln Tyr Ser Leu Ala Lys
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 Ser Tyr Ala Ser Thr Pro Glu Leu Arg Lys Thr Trp Leu Asp Ser Met
 930 935 940
 Ala Arg Ile His Val Lys Asn Gly Asp Leu Ser Glu Ala Ala Met Cys
 945 950 955 960
 Tyr Val His Val Thr Ala Leu Val Ala Glu Tyr Leu Thr Arg Lys Gly
 965 970 975
 Val Phe Arg Gln Gly Cys Thr Ala Phe Arg Val Ile Thr Pro Asn Ile
 980 985 990

Asp Glu Glu Ala Ser Met Met Glu Asp Val Gly Met Gln Asp Val His
 995 1000 1005
 Phe Asn Glu Asp Val Leu Met Glu Leu Leu Glu Gln Cys Ala Asp Gly
 1010 1015 1020
 Leu Trp Lys Ala Glu Arg Tyr Glu Leu Ile Ala Asp Ile Tyr Lys Leu
 1025 1030 1035 1040
 Ile Ile Pro Ile Tyr Glu Lys Arg Arg Asp Phe Phe Glu Asp Glu Asp
 1045 1050 1055
 Gly Lys Glu Tyr Ile Tyr Lys Glu Pro Lys Leu Thr Pro Leu Ser Glu
 1060 1065 1070
 Ile Ser Gln Arg Leu Leu Lys Leu Tyr Ser Asp Lys Phe Gly Ser Glu
 1075 1080 1085
 Asn Val Lys Met Ile Gln Asp Ser Gly Lys Val Asn Pro Lys Asp Leu
 1090 1095 1100
 Asp Ser Lys Tyr Ala Tyr Ile Gln Val Thr His Val Ile Pro Phe Phe
 1105 1110 1115 1120
 Asp Glu Lys Glu Leu Gln Glu Arg Lys Thr Glu Phe Glu Arg Ser His
 1125 1130 1135
 Asn Ile Arg Arg Phe Met Phe Glu Met Pro Phe Thr Gln Thr Gly Lys
 1140 1145 1150
 Arg Gln Gly Gly Val Glu Glu Gln Cys Lys Arg Arg Thr Ile Leu Thr
 1155 1160 1165
 Ala Ile His Cys Phe Pro Tyr Val Lys Lys Arg Ile Pro Val Met Tyr
 1170 1175 1180
 Gln His His Thr Asp Leu Asn Pro Ile Glu Val Ala Ile Asp Glu Met
 1185 1190 1195 1200
 Ser Lys Lys Val Ala Glu Leu Arg Gln Leu Cys Ser Ser Ala Glu Val
 1205 1210 1215
 Asp Met Ile Lys Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Gln
 1220 1225 1230
 Val Asn Ala Gly Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asp Asp Thr
 1235 1240 1245
 Asn Thr Lys Arg Tyr Pro Asp Asn Lys Val Lys Leu Leu Lys Glu Val
 1250 1255 1260
 Phe Arg Gln Phe Val Glu Ala Cys Gly Gln Ala Leu Ala Val Asn Glu
 1265 1270 1275 1280
 Arg Leu Ile Lys Glu Asp Gln Leu Glu Tyr Gln Glu Glu Met Lys Ala
 1285 1290 1295
 Asn Tyr Arg Glu Met Ala Lys Glu Leu Ser Glu Ile Met His Glu Gln
 1300 1305 1310

Ile Cys Pro Leu Glu Glu Lys Thr Ser Val Leu Pro Asn Ser Leu His
 1315 1320 1325

Ile Phe Asn Ala Ile Ser Gly Thr Pro Thr Ser Thr Met Val His Gly
 1330 1335 1340

Met Thr Ser Ser Ser Ser Val Val
 1345 1350

<210> 10
 <211> 1534
 <212> PRT
 <213> Homo sapiens

<220>
 <223> human KIAA1058

<400> 10
 Ala Ser Gly Asn Leu Asp Lys Asn Ala Arg Phe Ser Ala Ile Tyr Arg
 1 5 10 15

Gln Asp Ser Asn Lys Leu Ser Asn Asp Asp Met Leu Lys Leu Leu Ala
 20 25 30

Asp Phe Arg Lys Pro Glu Lys Met Ala Lys Leu Pro Val Ile Leu Gly
 35 40 45

Asn Leu Asp Ile Thr Ile Asp Asn Val Ser Ser Asp Phe Pro Asn Tyr
 50 55 60

Val Asn Ser Ser Tyr Ile Pro Thr Lys Gln Phe Glu Thr Cys Ser Lys
 65 70 75 80

Thr Pro Ile Thr Phe Glu Val Glu Glu Phe Val Pro Cys Ile Pro Lys
 85 90 95

His Thr Gln Pro Tyr Thr Ile Tyr Thr Asn His Leu Tyr Val Tyr Pro
 100 105 110

Lys Tyr Leu Lys Tyr Asp Ser Gln Lys Ser Phe Ala Lys Ala Arg Asn
 115 120 125

Ile Ala Ile Cys Ile Glu Phe Lys Asp Ser Asp Glu Glu Asp Ser Gln
 130 135 140

Pro Leu Lys Cys Ile Tyr Gly Arg Pro Gly Gly Pro Val Phe Thr Arg
 145 150 155 160

Ser Ala Phe Ala Ala Val Leu His His His Gln Asn Pro Glu Phe Tyr
 165 170 175

Asp Glu Ile Lys Ile Glu Leu Pro Thr Gln Leu His Glu Lys His His
 180 185 190

Leu Leu Leu Thr Phe Phe His Val Ser Cys Asp Asn Ser Ser Lys Gly
 195 200 205

Ser Thr Lys Lys Arg Asp Val Val Glu Thr Gln Val Gly Tyr Ser Trp
 210 215 220

Leu Pro Leu Leu Lys Asp Gly Arg Val Val Thr Ser Glu Gln His Ile
 225 230 235 240
 Pro Val Ser Ala Asn Leu Pro Ser Gly Tyr Leu Gly Tyr Gln Glu Leu
 245 250 255
 Gly Met Gly Arg His Tyr Gly Pro Glu Ile Lys Trp Val Asp Gly Gly
 260 265 270
 Lys Pro Leu Leu Lys Ile Ser Thr His Leu Val Ser Thr Val Tyr Thr
 275 280 285
 Gln Asp Gln His Leu His Asn Phe Phe Gln Tyr Cys Gln Lys Thr Glu
 290 295 300
 Ser Gly Ala Gln Ala Leu Gly Asn Glu Leu Val Lys Tyr Leu Lys Ser
 305 310 315 320
 Leu His Ala Met Glu Gly His Val Met Ile Ala Phe Leu Pro Thr Ile
 325 330 335
 Leu Asn Gln Leu Phe Arg Val Leu Thr Arg Ala Thr Gln Glu Glu Val
 340 345 350
 Ala Val Asn Val Thr Arg Val Ile Ile His Val Val Ala Gln Cys His
 355 360 365
 Glu Glu Gly Leu Glu Ser His Leu Arg Ser Tyr Val Lys Tyr Ala Tyr
 370 375 380
 Lys Ala Glu Pro Tyr Val Ala Ser Glu Tyr Lys Thr Val His Glu Glu
 385 390 395 400
 Leu Thr Lys Ser Met Thr Thr Ile Leu Lys Pro Ser Ala Asp Phe Leu
 405 410 415
 Thr Ser Asn Lys Leu Leu Lys Tyr Ser Trp Phe Phe Phe Asp Val Leu
 420 425 430
 Ile Lys Ser Met Ala Gln His Leu Ile Glu Asn Ser Lys Val Lys Leu
 435 440 445
 Leu Arg Asn Gln Arg Phe Pro Ala Ser Tyr His His Ala Val Glu Thr
 450 455 460
 Val Val Asn Met Leu Met Pro His Ile Thr Gln Lys Phe Arg Asp Asn
 465 470 475 480
 Pro Glu Ala Ser Lys Asn Ala Asn His Ser Leu Ala Val Phe Ile Lys
 485 490 495
 Arg Cys Phe Thr Phe Met Asp Arg Gly Phe Val Phe Lys Gln Ile Asn
 500 505 510
 Asn Tyr Ile Ser Cys Phe Ala Pro Gly Asp Pro Lys Thr Leu Phe Glu
 515 520 525
 Tyr Lys Phe Glu Phe Leu Arg Val Val Cys Asn His Glu His Tyr Ile
 530 535 540

Pro Leu Asn Leu Pro Met Pro Phe Gly Lys Gly Arg Ile Gln Arg Tyr
 545 550 555 560
 Gln Asp Leu Gln Leu Asp Tyr Ser Leu Thr Asp Glu Phe Cys Arg Asn
 565 570 575
 His Phe Leu Val Gly Leu Leu Leu Arg Glu Val Gly Thr Ala Leu Gln
 580 585 590
 Glu Phe Arg Glu Val Arg Leu Ile Ala Ile Ser Val Leu Lys Asn Leu
 595 600 605
 Leu Ile Lys His Ser Phe Asp Asp Arg Tyr Ala Ser Arg Ser His Gln
 610 615 620
 Ala Arg Ile Ala Thr Leu Tyr Leu Pro Leu Phe Gly Leu Leu Ile Glu
 625 630 635 640
 Asn Val Gln Arg Ile Asn Val Arg Asp Val Ser Pro Phe Pro Val Asn
 645 650 655
 Ala Gly Met Thr Val Lys Asp Glu Ser Leu Ala Leu Pro Ala Val Asn
 660 665 670
 Pro Leu Val Thr Pro Gln Lys Gly Ser Thr Leu Asp Asn Ser Leu His
 675 680 685
 Lys Asp Leu Leu Gly Ala Ile Ser Gly Ile Ala Ser Pro Tyr Thr Thr
 690 695 700
 Ser Thr Pro Asn Ile Asn Ser Val Arg Asn Ala Asp Ser Arg Gly Ser
 705 710 715 720
 Leu Ile Ser Thr Asp Ser Gly Asn Ser Leu Pro Glu Arg Asn Ser Glu
 725 730 735
 Lys Ser Asn Ser Leu Asp Lys His Gln Gln Ser Ser Thr Leu Gly Asn
 740 745 750
 Ser Val Val Arg Cys Asp Lys Leu Asp Gln Ser Glu Ile Lys Ser Leu
 755 760 765
 Leu Met Cys Phe Leu Tyr Ile Leu Lys Ser Met Ser Asp Asp Ala Leu
 770 775 780
 Phe Thr Tyr Trp Asn Lys Ala Ser Thr Ser Glu Leu Met Asp Phe Phe
 785 790 795 800
 Thr Ile Ser Glu Val Cys Leu His Gln Phe Gln Tyr Met Gly Lys Arg
 805 810 815
 Tyr Ile Ala Arg Thr Gly Met Met His Ala Arg Leu Gln Gln Leu Gly
 820 825 830
 Ser Leu Asp Asn Ser Leu Thr Phe Asn His Ser Tyr Gly His Ser Asp
 835 840 845
 Ala Asp Val Leu His Gln Ser Leu Leu Glu Ala Asn Ile Ala Thr Glu
 850 855 860

Val Cys Leu Thr Ala Leu Asp Thr Leu Ser Leu Phe Thr Leu Ala Phe
865 870 875 880
Lys Asn Gln Leu Leu Ala Asp His Gly His Asn Pro Leu Met Lys Lys
885 890 895
Val Phe Asp Val Tyr Leu Cys Phe Leu Gln Lys His Gln Ser Glu Thr
900 905 910
Ala Leu Lys Asn Val Phe Thr Ala Leu Arg Ser Leu Ile Tyr Lys Phe
915 920 925
Pro Ser Thr Phe Tyr Glu Gly Arg Ala Asp Met Cys Ala Ala Leu Cys
930 935 940
Tyr Glu Ile Leu Lys Cys Cys Asn Ser Lys Leu Ser Ser Ile Arg Thr
945 950 955 960
Glu Ala Ser Gln Leu Leu Tyr Phe Leu Met Arg Asn Asn Phe Asp Tyr
965 970 975
Thr Gly Lys Lys Ser Phe Val Arg Thr His Leu Gln Val Ile Ile Ser
980 985 990
Val Ser Gln Leu Ile Ala Asp Val Val Gly Ile Gly Gly Thr Arg Phe
995 1000 1005
Gln Gln Ser Leu Ser Ile Ile Asn Asn Cys Ala Asn Ser Asp Arg Leu
1010 1015 1020
Ile Lys His Thr Ser Phe Ser Ser Asp Val Lys Asp Leu Thr Lys Arg
1025 1030 1035 1040
Ile Arg Thr Val Leu Met Ala Thr Ala Gln Met Lys Glu His Glu Asn
1045 1050 1055
Asp Pro Glu Met Leu Val Asp Leu Gln Tyr Ser Leu Ala Lys Ser Tyr
1060 1065 1070
Ala Ser Thr Pro Glu Leu Arg Lys Thr Trp Leu Asp Ser Met Ala Arg
1075 1080 1085
Ile His Val Lys Asn Gly Asp Leu Ser Glu Ala Ala Met Cys Tyr Val
1090 1095 1100
His Val Thr Ala Leu Val Ala Glu Tyr Leu Thr Arg Lys Glu Ala Val
1105 1110 1115 1120
Gln Trp Glu Pro Pro Leu Leu Pro His Ser His Ser Ala Cys Leu Arg
1125 1130 1135
Arg Ser Arg Gly Gly Val Phe Arg Gln Gly Cys Thr Ala Phe Arg Val
1140 1145 1150
Ile Thr Pro Asn Ile Asp Glu Glu Ala Ser Met Met Glu Asp Val Gly
1155 1160 1165
Met Gln Asp Val His Phe Asn Glu Asp Val Leu Met Glu Leu Leu Glu
1170 1175 1180

Gln Cys Ala Asp Gly Leu Trp Lys Ala Glu Arg Tyr Glu Leu Ile Ala
 1185 1190 1195 1200
 Asp Ile Tyr Lys Leu Ile Ile Pro Ile Tyr Glu Lys Arg Arg Asp Phe
 1205 1210 1215
 Glu Arg Leu Ala His Leu Tyr Asp Thr Leu His Arg Ala Tyr Ser Lys
 1220 1225 1230
 Val Thr Glu Val Met His Ser Gly Arg Arg Leu Leu Gly Thr Tyr Phe
 1235 1240 1245
 Arg Val Ala Phe Phe Gly Gln Ala Ala Gln Tyr Gln Phe Thr Asp Ser
 1250 1255 1260
 Glu Thr Asp Val Glu Gly Phe Phe Glu Asp Glu Asp Gly Lys Glu Tyr
 1265 1270 1275 1280
 Ile Tyr Lys Glu Pro Lys Leu Thr Pro Leu Ser Glu Ile Ser Gln Arg
 1285 1290 1295
 Leu Leu Lys Leu Tyr Ser Asp Lys Phe Gly Ser Glu Asn Val Lys Met
 1300 1305 1310
 Ile Gln Asp Ser Gly Lys Val Asn Pro Lys Asp Leu Asp Ser Lys Tyr
 1315 1320 1325
 Ala Tyr Ile Gln Val Thr His Val Ile Pro Phe Phe Asp Glu Lys Glu
 1330 1335 1340
 Leu Gln Glu Arg Lys Thr Glu Phe Glu Arg Ser His Asn Ile Arg Arg
 1345 1350 1355 1360
 Phe Met Phe Glu Met Pro Phe Thr Gln Thr Gly Lys Arg Gln Gly Gly
 1365 1370 1375
 Val Glu Glu Gln Cys Lys Arg Arg Thr Ile Leu Thr Ala Ile His Cys
 1380 1385 1390
 Phe Pro Tyr Val Lys Lys Arg Ile Pro Val Met Tyr Gln His His Thr
 1395 1400 1405
 Asp Leu Asn Pro Ile Glu Val Ala Ile Asp Glu Met Ser Lys Lys Val
 1410 1415 1420
 Ala Glu Leu Arg Gln Leu Cys Ser Ser Ala Glu Val Asp Met Ile Lys
 1425 1430 1435 1440
 Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Gln Val Asn Ala Gly
 1445 1450 1455
 Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asp Asp Thr Asn Thr Lys Arg
 1460 1465 1470
 Tyr Pro Asp Asn Lys Val Lys Leu Leu Lys Glu Val Phe Arg Gln Phe
 1475 1480 1485
 Val Glu Ala Cys Gly Gln Ala Leu Ala Val Asn Glu Arg Leu Ile Lys
 1490 1495 1500

Glu Asp Gln Leu Glu Tyr Gln Glu Glu Met Lys Ala Asn Tyr Arg Glu
 1505 1510 1515 1520

Met Ala Lys Glu Leu Ser Glu Ile Met His Glu Gln Leu Gly
 1525 1530

<210> 11
 <211> 738
 <212> PRT
 <213> Rattus norvegicus

<220>
 <223> rat TRG

<400> 11
 Lys Leu Ser Arg Gly His Ser Pro Leu Met Lys Lys Val Phe Asp Val
 1 5 10 15
 Tyr Leu Cys Phe Leu Gln Lys His Gln Ser Glu Met Ala Leu Lys Asn
 20 25 30
 Val Phe Thr Ala Leu Arg Ser Leu Ile Tyr Lys Phe Pro Ser Thr Phe
 35 40 45
 Tyr Glu Gly Arg Ala Asp Met Cys Ala Ser Leu Cys Tyr Glu Val Leu
 50 55 60
 Lys Cys Cys Asn Ser Lys Leu Ser Ser Ile Arg Thr Glu Ala Ser Gln
 65 70 75 80
 Leu Leu Tyr Phe Leu Met Arg Asn Asn Phe Asp Tyr Thr Gly Lys Lys
 85 90 95
 Ser Phe Val Arg Thr His Leu Gln Val Ile Ile Ser Leu Ser Gln Leu
 100 105 110
 Ile Ala Asp Val Val Gly Ile Gly Gly Thr Arg Phe Gln Gln Ser Leu
 115 120 125
 Ser Ile Ile Asn Asn Cys Ala Asn Ser Asp Arg Leu Ile Lys His Thr
 130 135 140
 Ser Phe Ser Ser Asp Val Lys Asp Leu Thr Lys Arg Ile Arg Thr Val
 145 150 155 160
 Leu Met Ala Thr Ala Gln Met Lys Glu His Glu Asn Asp Pro Glu Met
 165 170 175
 Leu Val Asp Leu Gln Tyr Ser Leu Ala Lys Ser Tyr Ala Ser Thr Pro
 180 185 190
 Glu Leu Arg Lys Thr Trp Leu Asp Ser Met Ala Arg Ile His Val Lys
 195 200 205
 Asn Gly Asp Leu Ser Glu Ala Ala Met Cys Tyr Val His Val Thr Ala
 210 215 220
 Leu Val Ala Glu Tyr Leu Thr Arg Lys Glu Ala Asp Leu Ala Leu Gln
 225 230 235 240

Arg Glu Pro Pro Val Phe Pro Tyr Ser His Thr Ser Cys Gln Arg Lys
 245 250 255
 Ser Arg Gly Gly Met Phe Arg Gln Gly Cys Thr Ala Phe Arg Val Ile
 260 265 270
 Thr Pro Asn Ile Asp Glu Glu Ala Ser Met Met Glu Asp Val Gly Met
 275 280 285
 Gln Asp Val His Phe Asn Glu Asp Val Leu Met Glu Leu Leu Glu Gln
 290 295 300
 Cys Ala Asp Gly Leu Trp Lys Ala Glu Arg Leu Arg Ala Gly Leu Leu
 305 310 315 320
 Thr Ser Ile Asn Ser Ser Ser Pro Ser Met Lys Ser Gly Gly Thr Leu
 325 330 335
 Glu Thr Thr His Leu Tyr Asp Thr Leu His Arg Pro Tyr Ser Lys Val
 340 345 350
 Thr Glu Val Ile Thr Arg Ala Ala Gly Ser Trp Asp Leu Leu Pro Gly
 355 360 365
 Gly Leu Phe Gly Gln Gly Phe Phe Glu Asp Glu Asp Gly Lys Glu Tyr
 370 375 380
 Ile Tyr Lys Glu Pro Lys Leu Thr Pro Leu Ser Glu Ile Ser Gln Arg
 385 390 395 400
 Leu Leu Lys Leu Tyr Ser Asp Lys Phe Gly Ser Glu Asn Val Lys Met
 405 410 415
 Ile Gln Asp Ser Gly Lys Val Asn Pro Lys Asp Leu Asp Ser Lys Phe
 420 425 430
 Ala Tyr Ile Gln Val Thr His Val Thr Pro Phe Phe Asp Glu Lys Glu
 435 440 445
 Leu Gln Glu Arg Lys Thr Glu Phe Glu Arg Cys His Asn Ile Arg Arg
 450 455 460
 Phe Met Phe Glu Met Pro Phe Thr Gln Thr Gly Lys Arg Gln Gly Gly
 465 470 475 480
 Val Glu Glu Gln Cys Lys Arg Arg Thr Ile Leu Thr Ala Ile His Cys
 485 490 495
 Phe Pro Tyr Val Lys Lys Arg Ile Pro Val Met Tyr Gln His His Thr
 500 505 510
 Asp Leu Asn Pro Ile Glu Val Ala Ile Asp Glu Met Ser Lys Lys Val
 515 520 525
 Ala Glu Leu His Gln Leu Cys Ser Ser Ala Glu Val Asp Met Ile Lys
 530 535 540
 Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Gln Val Asn Ala Gly
 545 550 555 560

Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asp Asp Thr Asn Thr Lys Arg
 565 570 575
 Tyr Pro Asp Asn Lys Val Lys Leu Leu Lys Glu Val Phe Arg Gln Phe
 580 585 590
 Val Glu Ala Cys Gly Gln Ala Leu Ala Val Asn Glu Arg Leu Ile Lys
 595 600 605
 Glu Asp Gln Leu Glu Tyr Gln Glu Glu Met Lys Ala Asn Tyr Arg Glu
 610 615 620
 Ile Arg Lys Glu Leu Ser Asp Ile Ile Val Pro Arg Ile Cys Pro Gly
 625 630 635 640
 Glu Asp Lys Arg Ala Thr Lys Phe Pro Ala His Leu Gln Arg His Gln
 645 650 655
 Arg Asp Thr Asn Lys His Ser Gly Ser Arg Val Asp Gln Phe Ile Leu
 660 665 670
 Ser Cys Val Thr Leu Pro His Glu Pro His Val Gly Thr Cys Phe Val
 675 680 685
 Met Cys Lys Leu Arg Thr Thr Phe Arg Ala Asn His Trp Phe Cys Gln
 690 695 700
 Ala Gln Glu Glu Ala Met Gly Asn Gly Arg Glu Lys Glu Pro Trp Thr
 705 710 715 720
 Val Ile Phe Asn Ser Arg Phe Tyr Arg Ser Trp Gly Lys Val His Ile
 725 730 735

Phe Phe

<210> 12
 <211> 1214
 <212> PRT
 <213> Homo sapiens

<220>
 <223> human CLASP-4

<400> 12
 Met Glu Ile Gln Val Leu Ile Arg Phe Leu Ser Val Ile Leu Met Gln
 1 5 10 15
 Leu Phe Trp Val Leu Pro Asn Met Ile His Glu Asp Asp Val Pro Ile
 20 25 30
 Ser Cys Pro Met Val Leu Phe His Ile Val Ser Lys Cys His Glu Glu
 35 40 45
 Gly Leu Asp Ser Tyr Leu Ser Ser Phe Ile Lys Tyr Ser Phe Arg Pro
 50 55 60
 Gly Lys Pro Ser Ala Pro Gln Ala Pro Leu Ile His Glu Thr Leu Ala
 65 70 75 80

Thr Met Met Ile Ala Leu Leu Lys Gln Ser Ala Asp Phe Leu Ala Ile
 85 90 95
 Asn Lys Leu Leu Lys Tyr Ser Trp Phe Phe Phe Glu Ile Ile Ala Lys
 100 105 110
 Ser Met Ala Thr Tyr Leu Leu Glu Glu Asn Lys Ile Lys Leu Thr His
 115 120 125
 Gly Gln Arg Phe Pro Lys Ala Tyr His His Ala Leu His Ser Leu Phe
 130 135 140
 Leu Ala Ile Thr Ile Val Glu Ser Gln Tyr Ala Glu Ile Pro Lys Glu
 145 150 155 160
 Ser Arg Asn Val Asn Tyr Ser Leu Ala Ser Phe Leu Lys Cys Cys Leu
 165 170 175
 Thr Leu Met Asp Arg Gly Phe Val Phe Asn Leu Ile Asn Asp Tyr Ile
 180 185 190
 Ser Gly Phe Ser Pro Lys Asp Pro Lys Val Leu Ala Glu Tyr Lys Phe
 195 200 205
 Glu Phe Leu Gln Thr Ile Cys Asn His Glu His Tyr Ile Pro Leu Asn
 210 215 220
 Leu Pro Met Ala Phe Ala Lys Pro Lys Leu Gln Arg Val Gln Asp Ser
 225 230 235 240
 Asn Leu Glu Tyr Ser Leu Ser Asp Glu Tyr Cys Lys His His Phe Leu
 245 250 255
 Val Gly Leu Leu Leu Arg Glu Thr Ser Ile Ala Leu Gln Asp Asn Tyr
 260 265 270
 Glu Ile Arg Tyr Thr Ala Ile Ser Val Ile Lys Asn Leu Leu Ile Lys
 275 280 285
 His Ala Phe Asp Thr Arg Tyr Gln His Lys Asn Gln Gln Ala Lys Ile
 290 295 300
 Ala Gln Leu Tyr Leu Pro Phe Val Gly Leu Leu Leu Glu Asn Ile Gln
 305 310 315 320
 Arg Leu Ala Gly Arg Asp Thr Leu Tyr Ser Cys Ala Ala Met Pro Asn
 325 330 335
 Ser Ala Ser Arg Asp Glu Phe Pro Cys Gly Phe Thr Ser Pro Ala Asn
 340 345 350
 Arg Gly Ser Leu Ser Thr Asp Lys Asp Thr Ala Tyr Gly Ser Phe Gln
 355 360 365
 Asn Gly His Gly Ile Lys Arg Glu Asp Ser Arg Gly Ser Leu Ile Pro
 370 375 380
 Glu Gly Ala Thr Gly Phe Pro Asp Gln Gly Asn Thr Gly Glu Asn Thr
 385 390 395 400

Arg Gln Ser Ser Thr Arg Ser Ser Val Ser Gln Tyr Asn Arg Leu Asp
 405 410 415
 Gln Tyr Glu Ile Arg Ser Leu Leu Met Cys Tyr Leu Tyr Ile Val Lys
 420 425 430
 Met Ile Ser Glu Asp Thr Leu Leu Thr Tyr Trp Asn Lys Val Ser Pro
 435 440 445
 Gln Glu Leu Ile Asn Ile Leu Ile Leu Leu Glu Val Cys Leu Phe His
 450 455 460
 Phe Arg Tyr Met Gly Lys Arg Asn Ile Ala Arg Val His Asp Ala Trp
 465 470 475 480
 Leu Ser Lys His Phe Gly Ile Asp Arg Lys Ser Gln Thr Met Pro Ala
 485 490 495
 Leu Arg Asn Arg Ser Gly Val Met Gln Ala Arg Leu Gln His Leu Ser
 500 505 510
 Ser Leu Glu Ser Ser Phe Thr Leu Asn His Ser Ser Thr Thr Thr Glu
 515 520 525
 Ala Asp Ile Phe His Gln Ala Leu Leu Glu Gly Asn Thr Ala Thr Glu
 530 535 540
 Val Ser Leu Thr Val Leu Asp Thr Ile Ser Phe Phe Thr Gln Cys Phe
 545 550 555 560
 Lys Thr His Phe Leu Asn Asn Asp Gly His Asn Pro Leu Met Lys Lys
 565 570 575
 Val Phe Asp Ile His Leu Ala Phe Leu Lys Asn Gly Gln Ser Glu Val
 580 585 590
 Ser Leu Lys His Val Phe Ala Ser Leu Arg Ala Phe Ile Ser Lys Phe
 595 600 605
 Pro Ser Ala Phe Phe Lys Gly Arg Val Asn Met Cys Ala Ala Phe Cys
 610 615 620
 Tyr Glu Val Leu Lys Cys Cys Thr Ser Lys Ile Ser Ser Thr Arg Asn
 625 630 635 640
 Glu Ala Ser Ala Leu Leu Tyr Leu Leu Met Arg Asn Asn Phe Glu Tyr
 645 650 655
 Thr Lys Arg Lys Thr Phe Leu Arg Thr His Leu Gln Ile Ile Ile Ala
 660 665 670
 Val Ser Gln Leu Ile Ala Asp Val Ala Leu Ser Gly Gly Ser Arg Phe
 675 680 685
 Gln Glu Ser Leu Phe Ile Ile Asn Asn Phe Ala Asn Ser Asp Arg Pro
 690 695 700
 Met Leu Ala Arg Ala Phe Pro Ala Glu Val Lys Asp Leu Thr Lys Arg
 705 710 715 720

Ile	Arg	Thr	Val	Leu	Met	Ala	Thr	Ala	Gln	Met	Lys	Glu	His	Glu	Lys	725	730	735
Asp	Pro	Glu	Met	Leu	Ile	Asp	Leu	Gln	Tyr	Ser	Leu	Ala	Lys	Ser	Tyr	740	745	750
Ala	Ser	Thr	Pro	Glu	Leu	Arg	Lys	Thr	Trp	Leu	Asp	Ser	Met	Ala	Lys	755	760	765
Ile	His	Val	Lys	Asn	Gly	Asp	Phe	Ser	Glu	Ala	Ala	Met	Cys	Tyr	Val	770	775	780
His	Val	Ala	Ala	Leu	Val	Ala	Glu	Phe	Leu	His	Arg	Lys	Lys	Leu	Phe	785	790	795
Pro	Asn	Gly	Cys	Ser	Ala	Phe	Lys	Lys	Ile	Thr	Pro	Asn	Ile	Asp	Glu	805	810	815
Glu	Gly	Ala	Met	Lys	Glu	Asp	Ala	Gly	Met	Met	Asp	Val	His	Tyr	Ser	820	825	830
Glu	Glu	Val	Leu	Leu	Glu	Leu	Leu	Glu	Gln	Cys	Val	Asn	Gly	Leu	Trp	835	840	845
Lys	Ala	Glu	Arg	Tyr	Glu	Ile	Ile	Ser	Glu	Ile	Ser	Lys	Leu	Ile	Gly	850	855	860
Pro	Ile	Tyr	Glu	Asn	Arg	Arg	Glu	Phe	Glu	Asn	Leu	Thr	Gln	Val	Tyr	865	870	875
Arg	Thr	Leu	His	Gly	Ala	Tyr	Thr	Lys	Ile	Leu	Glu	Val	Met	His	Thr	885	890	895
Lys	Lys	Arg	Leu	Leu	Gly	Thr	Phe	Phe	Arg	Val	Ala	Phe	Tyr	Gly	Gln	900	905	910
Ser	Phe	Phe	Glu	Glu	Glu	Asp	Gly	Lys	Glu	Tyr	Ile	Tyr	Lys	Glu	Pro	915	920	925
Lys	Leu	Thr	Gly	Leu	Ser	Glu	Ile	Ser	Leu	Arg	Leu	Val	Lys	Leu	Tyr	930	935	940
Gly	Glu	Lys	Phe	Gly	Thr	Glu	Asn	Val	Lys	Ile	Ile	Gln	Asp	Ser	Asp	945	950	955
Lys	Val	Asn	Ala	Lys	Glu	Leu	Asp	Pro	Lys	Tyr	Ala	His	Ile	Gln	Val	965	970	975
Thr	Tyr	Val	Lys	Pro	Tyr	Phe	Asp	Asp	Lys	Glu	Leu	Thr	Glu	Arg	Lys	980	985	990
Thr	Glu	Phe	Glu	Arg	Asn	His	Asn	Ile	Ser	Arg	Phe	Val	Phe	Glu	Ala	995	1000	1005
Pro	Tyr	Thr	Leu	Ser	Gly	Lys	Lys	Gln	Gly	Cys	Ile	Glu	Glu	Gln	Cys	1010	1015	1020
Lys	Arg	Arg	Thr	Ile	Leu	Thr	Thr	Ser	Asn	Ser	Phe	Pro	Tyr	Val	Lys	1025	1030	1035

Lys Arg Ile Pro Ile Asn Cys Glu Gln Gln Ile Asn Leu Lys Pro Ile
 1045 1050 1055
 Asp Gly Ala Thr Asp Glu Ile Lys Asp Lys Thr Ala Glu Leu Gln Lys
 1060 1065 1070
 Leu Cys Ser Ser Thr Asp Val Asp Met Ile Gln Leu Gln Leu Lys Leu
 1075 1080 1085
 Gln Gly Trp Val Ser Val Gln Val Asn Ala Gly Pro Leu Ala Tyr Ala
 1090 1095 1100
 Arg Ala Phe Leu Asn Asp Ser Gln Ala Ser Lys Tyr Pro Pro Lys Lys
 1105 1110 1115 1120
 Val Ser Glu Leu Lys Asp Met Phe Arg Lys Phe Ile Gln Ala Cys Ser
 1125 1130 1135
 Ile Ala Leu Glu Leu Asn Glu Arg Leu Ile Lys Glu Asp Gln Val Glu
 1140 1145 1150
 Tyr His Glu Gly Leu Lys Ser Asn Phe Arg Asp Met Val Lys Glu Leu
 1155 1160 1165
 Ser Asp Ile Ile His Glu Gln Ile Leu Gln Glu Asp Thr Met His Ser
 1170 1175 1180
 Pro Trp Met Ser Asn Thr Leu His Val Phe Cys Ala Ile Ser Gly Thr
 1185 1190 1195 1200
 Ser Ser Asp Arg Gly Tyr Gly Ser Pro Arg Tyr Ala Glu Val
 1205 1210

<210> 13
 <211> 1288
 <212> PRT
 <213> Homo sapiens

<220>
 <223> human CLASP-1

<400> 13
 Met Ser Phe Leu Pro Ile Ile Leu Asn Gln Leu Phe Lys Val Leu Val
 1 5 10 15
 Gln Asn Glu Glu Asp Glu Ile Thr Thr Thr Val Thr Arg Val Leu Pro
 20 25 30
 Asp Ile Val Ala Lys Cys His Glu Glu Gln Leu Asp His Ser Val Gln
 35 40 45
 Ser Tyr Ile Lys Phe Val Phe Lys Thr Arg Ala Cys Lys Glu Arg Pro
 50 55 60
 Val His Glu Asp Leu Ala Lys Asn Val Thr Gly Leu Leu Lys Ser Asn
 65 70 75 80
 Asp Ser Pro Thr Val Lys His Val Leu Lys His Ser Trp Phe Phe Phe
 85 90 95

Ala Ile Ile Leu Lys Ser Met Ala Gln His Leu Ile Asp Thr Asn Lys
 100 105 110
 Ile Gln Leu Pro Arg Pro Gln Arg Phe Pro Glu Ser Tyr Gln Asn Glu
 115 120 125
 Leu Asp Asn Leu Val Met Val Leu Ser Asp His Val Ile Trp Lys Tyr
 130 135 140
 Lys Asp Ala Leu Glu Glu Thr Arg Arg Ala Thr His Ser Val Ala Arg
 145 150 155 160
 Phe Leu Lys Arg Cys Phe Thr Phe Met Asp Arg Gly Cys Val Phe Lys
 165 170 175
 Met Val Asn Asn Tyr Ile Ser Met Phe Ser Ser Gly Asp Leu Lys Thr
 180 185 190
 Leu Cys Gln Tyr Lys Phe Asp Phe Leu Gln Glu Val Cys Gln His Glu
 195 200 205
 His Phe Ile Pro Leu Cys Leu Pro Ile Arg Ser Ala Asn Ile Pro Asp
 210 215 220
 Pro Leu Thr Pro Ser Glu Ser Thr Gln Glu Leu His Ala Ser Asp Met
 225 230 235 240
 Pro Glu Tyr Ser Val Thr Asn Glu Phe Cys Arg Lys His Phe Leu Ile
 245 250 255
 Gly Ile Leu Leu Arg Glu Val Gly Phe Ala Leu Gln Glu Asp Gln Asp
 260 265 270
 Val Arg His Leu Ala Leu Ala Val Leu Lys Asn Leu Met Ala Lys His
 275 280 285
 Ser Phe Asp Asp Arg Tyr Arg Glu Pro Arg Lys Gln Ala Gln Ile Ala
 290 295 300
 Ser Leu Tyr Met Pro Leu Tyr Gly Met Leu Leu Asp Asn Met Pro Arg
 305 310 315 320
 Ile Tyr Leu Lys Asp Leu Tyr Pro Phe Thr Val Asn Thr Ser Asn Gln
 325 330 335
 Gly Ser Arg Asp Asp Leu Ser Thr Asn Gly Gly Phe Gln Ser Gln Thr
 340 345 350
 Ala Ile Lys His Ala Asn Ser Val Asp Thr Ser Phe Ser Lys Asp Val
 355 360 365
 Leu Asn Ser Ile Ala Ala Phe Ser Ser Ile Ala Ile Ser Thr Val Asn
 370 375 380
 His Ala Asp Ser Arg Ala Ser Leu Ala Ser Leu Asp Ser Asn Pro Ser
 385 390 395 400
 Thr Asn Glu Lys Ser Ser Glu Lys Thr Asp Asn Cys Glu Lys Ile Pro
 405 410 415

Arg Pro Leu Ala Leu Ile Gly Ser Thr Leu Arg Phe Asp Arg Leu Asp
 420 425 430
 Gln Ala Glu Thr Arg Ser Leu Leu Met Cys Phe Leu His Ile Met Lys
 435 440 445
 Thr Ile Ser Tyr Glu Thr Leu Ile Ala Tyr Trp Gln Arg Ala Pro Ser
 450 455 460
 Pro Glu Val Ser Asp Phe Phe Ser Ile Leu Asp Val Cys Leu Gln Asn
 465 470 475 480
 Phe Arg Tyr Leu Gly Lys Arg Asn Ile Ile Arg Lys Ile Ala Ala Ala
 485 490 495
 Phe Lys Phe Val Gln Ser Thr Gln Asn Asn Gly Thr Leu Lys Gly Ser
 500 505 510
 Asn Pro Ser Cys Gln Thr Ser Gly Leu Leu Ala Gln Trp Met His Ser
 515 520 525
 Thr Ser Arg His Glu Gly His Lys Gln His Arg Ser Gln Thr Leu Pro
 530 535 540
 Ile Ile Arg Gly Lys Asn Ala Leu Ser Asn Pro Lys Leu Leu Gln Met
 545 550 555 560
 Leu Asp Asn Thr Met Thr Ser Asn Ser Asn Glu Ile Asp Ile Val His
 565 570 575
 His Val Asp Thr Glu Ala Asn Ile Ala Thr Glu Gly Cys Leu Thr Ile
 580 585 590
 Leu Asp Leu Val Ser Leu Phe Thr Gln Thr His Gln Arg Gln Leu Gln
 595 600 605
 Gln Cys Asp Cys Gln Asn Ser Leu Met Lys Arg Gly Phe Asp Thr Tyr
 610 615 620
 Met Leu Phe Phe Gln Val Asn Gln Ser Ala Thr Ala Leu Lys His Val
 625 630 635 640
 Phe Ala Ser Leu Arg Leu Phe Val Cys Lys Phe Pro Ser Ala Phe Phe
 645 650 655
 Gln Gly Pro Ala Asp Leu Cys Gly Ser Phe Cys Tyr Glu Val Leu Lys
 660 665 670
 Cys Cys Asn His Arg Ser Arg Ser Thr Gln Thr Glu Ala Ser Ala Leu
 675 680 685
 Leu Tyr Leu Phe Met Arg Lys Asn Phe Glu Phe Asn Lys Gln Lys Ser
 690 695 700
 Ile Val Arg Ser His Leu Gln Leu Ile Lys Ala Val Ser Gln Leu Ile
 705 710 715 720
 Ala Asp Ala Gly Ile Gly Gly Ser Arg Phe Gln His Ser Leu Ala Ile
 725 730 735

Thr Asn Asn Phe Ala Asn Gly Asp Lys Gln Met Lys Asn Ser Asn Phe
 740 745 750
 Pro Ala Glu Val Lys Asp Leu Thr Lys Arg Ile Arg Thr Val Leu Met
 755 760 765
 Ala Thr Ala Gln Met Lys Glu His Glu Lys Asp Pro Glu Met Leu Val
 770 775 780
 Asp Leu Gln Tyr Ser Leu Ala Asn Ser Tyr Ala Ser Thr Pro Glu Leu
 785 790 795 800
 Arg Arg Thr Trp Leu Glu Ser Met Ala Lys Ile His Ala Arg Asn Gly
 805 810 815
 Asp Leu Ser Glu Ala Ala Met Cys Tyr Ile His Ile Ala Ala Leu Ile
 820 825 830
 Ala Glu Tyr Leu Lys Arg Lys Gly Tyr Trp Lys Val Glu Lys Ile Cys
 835 840 845
 Thr Ala Ser Leu Leu Ser Glu Asp Thr His Pro Cys Asp Ser Asn Ser
 850 855 860
 Leu Leu Thr Thr Pro Ser Gly Gly Ser Met Phe Ser Met Gly Trp Pro
 865 870 875 880
 Ala Phe Leu Ser Ile Thr Pro Asn Ile Lys Glu Glu Gly Ala Ala Lys
 885 890 895
 Glu Asp Ser Gly Met His Asp Thr Pro Tyr Asn Glu Asn Ile Leu Val
 900 905 910
 Glu Gln Leu Tyr Met Cys Gly Glu Phe Leu Trp Lys Ser Glu Arg Tyr
 915 920 925
 Glu Leu Ile Ala Asp Val Asn Lys Pro Ile Ile Ala Val Phe Glu Lys
 930 935 940
 Gln Arg Asp Phe Lys Lys Leu Ser Asp Leu Tyr Tyr Asp Ile His Arg
 945 950 955 960
 Ser Tyr Leu Lys Val Ala Glu Val Val Asn Ser Glu Lys Arg Leu Phe
 965 970 975
 Gly Arg Tyr Tyr Arg Val Ala Phe Tyr Gly Gln Gly Phe Phe Glu Glu
 980 985 990
 Glu Glu Gly Lys Glu Tyr Ile Tyr Lys Glu Pro Lys Leu Thr Gly Leu
 995 1000 1005
 Ser Glu Ile Ser Gln Arg Leu Leu Lys Leu Tyr Ala Asp Lys Phe Gly
 1010 1015 1020
 Ala Asp Asn Val Lys Ile Ile Gln Asp Ser Asn Lys Val Asn Pro Lys
 1025 1030 1035 1040
 Asp Leu Asp Pro Lys Tyr Ala Tyr Ile Gln Val Thr Tyr Val Thr Pro
 1045 1050 1055

Phe Phe Glu Glu Lys Glu Ile Glu Asp Arg Lys Thr Asp Phe Glu Met
1060 1065 1070
His His Asn Ile Asn Arg Phe Val Phe Glu Thr Pro Phe Thr Leu Ser
1075 1080 1085
Gly Lys Lys His Gly Gly Val Ala Glu Gln Cys Lys Arg Arg Thr Ile
1090 1095 1100
Leu Thr Thr Ser His Leu Phe Pro Tyr Val Lys Lys Arg Ile Gln Val
1105 1110 1115 1120
Ile Ser Gln Ser Ser Thr Glu Leu Asn Pro Ile Glu Val Ala Ile Asp
1125 1130 1135
Glu Met Ser Arg Lys Val Ser Glu Leu Asn Gln Leu Cys Thr Met Glu
1140 1145 1150
Glu Val Asp Met Ile Ser Leu Gln Leu Lys Leu Gln Gly Ser Val Ser
1155 1160 1165
Val Lys Val Asn Ala Gly Pro Met Ala Tyr Ala Arg Ala Phe Leu Glu
1170 1175 1180
Glu Thr Asn Ala Lys Lys Tyr Pro Asp Asn Gln Val Lys Leu Leu Lys
1185 1190 1195 1200
Glu Ile Phe Arg Gln Phe Ala Asp Ala Cys Gly Gln Ala Leu Asp Val
1205 1210 1215
Asn Glu Arg Leu Ile Lys Glu Asp Gln Leu Glu Tyr Gln Glu Glu Leu
1220 1225 1230
Arg Ser His Tyr Lys Asp Met Leu Ser Glu Leu Ser Thr Val Met Asn
1235 1240 1245
Glu Gln Ile Thr Gly Arg Asp Asp Leu Ser Lys Arg Gly Val Asp Gln
1250 1255 1260
Thr Cys Thr Arg Val Ile Ser Lys Ala Thr Pro Ala Leu Pro Thr Val
1265 1270 1275 1280
Ser Ile Ser Ser Ser Ala Glu Val
1285

<210> 14

<211> 1220

<212> PRT

<213> Homo sapiens

<220>

<223> human CLASP-3

<400> 14

Gly Pro Gly Pro Ala Arg Ser Thr Val Ser Ile Ser Leu Ile Ser Asn
1 5 10 15

Ser Ala Arg Val Asn Arg Ser Arg Ser Leu Ser Asn Ser Asn Pro Asp
20 25 30

Ile Ser Gly Thr Pro Thr Ser Pro Asp Asp Glu Val Arg Ser Ile Ile
 35 40 45
 Gly Ser Lys Gly Leu Asp Arg Ser Asn Ser Trp Val Asn Thr Gly Gly
 50 55 60
 Pro Lys Ala Ala Pro Trp Gly Ser Asn Pro Ser Pro Ser Ala Glu Ser
 65 70 75 80
 Thr Gln Ala Met Asp Arg Ser Cys Asn Arg Met Ser Ser His Thr Glu
 85 90 95
 Thr Ser Ser Phe Leu Gln Thr Leu Thr Gly Arg Leu Pro Thr Lys Lys
 100 105 110
 Leu Phe His Glu Glu Leu Ala Leu Gln Trp Val Val Cys Ser Gly Ser
 115 120 125
 Val Arg Glu Ser Ala Leu Gln Gln Ala Trp Phe Phe Phe Glu Leu Met
 130 135 140
 Val Lys Ser Met Val His His Leu Tyr Phe Asn Asp Lys Leu Glu Ala
 145 150 155 160
 Pro Arg Lys Ser Arg Phe Pro Glu Arg Phe Met Asp Asp Ile Ala Ala
 165 170 175
 Leu Val Ser Thr Ile Ala Ser Asp Ile Val Ser Arg Phe Gln Lys Asp
 180 185 190
 Thr Glu Met Val Glu Arg Leu Asn Thr Ser Leu Ala Phe Phe Leu Asn
 195 200 205
 Asp Leu Leu Ser Val Met Asp Arg Gly Phe Val Phe Ser Leu Ile Lys
 210 215 220
 Ser Cys Tyr Lys Gln Val Ser Ser Lys Leu Tyr Ser Leu Pro Asn Pro
 225 230 235 240
 Ser Val Leu Val Ser Leu Arg Leu Asp Phe Leu Arg Ile Ile Cys Ser
 245 250 255
 His Glu His Tyr Val Thr Leu Asn Leu Pro Cys Ser Leu Leu Thr Pro
 260 265 270
 Pro Ala Ser Pro Ser Pro Ser Val Ser Ser Ala Thr Ser Gln Ser Ser
 275 280 285
 Gly Phe Ser Thr Asn Val Gln Asp Gln Lys Ile Ala Asn Met Phe Glu
 290 295 300
 Leu Ser Val Pro Phe Arg Gln Gln His Tyr Leu Ala Gly Leu Val Leu
 305 310 315 320
 Thr Glu Leu Ala Val Ile Leu Asp Pro Asp Ala Glu Gly Leu Phe Gly
 325 330 335
 Leu His Lys Lys Val Ile Asn Met Val His Asn Leu Leu Ser Ser His
 340 345 350

Asp	Ser	Asp	Pro	Arg	Tyr	Ser	Asp	Pro	Gln	Ile	Lys	Ala	Arg	Val	Ala		
		355					360					365					
Met	Leu	Tyr	Leu	Pro	Leu	Ile	Gly	Ile	Ile	Met	Glu	Thr	Val	Pro	Gln		
	370					375					380						
Leu	Tyr	Asp	Phe	Thr	Glu	Thr	His	Asn	Gln	Arg	Gly	Arg	Pro	Ile	Cys		
385					390					395					400		
Ile	Ala	Thr	Asp	Asp	Tyr	Glu	Ser	Glu	Ser	Gly	Ser	Met	Ile	Ser	Gln		
			405						410					415			
Thr	Val	Ala	Met	Ala	Ile	Ala	Gly	Thr	Ser	Val	Pro	Gln	Leu	Thr	Arg		
		420						425					430				
Pro	Gly	Ser	Phe	Leu	Leu	Thr	Ser	Thr	Ser	Gly	Arg	Gln	His	Thr	Thr		
	435						440					445					
Phe	Ser	Ala	Glu	Ser	Ser	Arg	Ser	Leu	Leu	Ile	Cys	Leu	Leu	Trp	Val		
450						455					460						
Leu	Lys	Asn	Ala	Asp	Glu	Thr	Val	Leu	Gln	Lys	Trp	Phe	Thr	Asp	Leu		
465					470					475					480		
Ser	Val	Leu	Gln	Leu	Asn	Arg	Leu	Leu	Asp	Leu	Leu	Tyr	Leu	Cys	Val		
			485						490					495			
Ser	Cys	Phe	Glu	Tyr	Lys	Gly	Lys	Lys	Val	Phe	Glu	Arg	Met	Asn	Ser		
		500					505						510				
Leu	Thr	Phe	Lys	Lys	Ser	Lys	Asp	Met	Arg	Ala	Lys	Leu	Glu	Glu	Ala		
	515						520					525					
Ile	Leu	Gly	Ser	Ile	Gly	Ala	Arg	Gln	Glu	Met	Val	Arg	Arg	Ser	Arg		
530						535					540						
Gly	Gln	Leu	Glu	Arg	Ser	Pro	Ser	Gly	Ser	Ala	Phe	Gly	Ser	Gln	Glu		
545					550					555					560		
Asn	Leu	Arg	Trp	Arg	Lys	Asp	Met	Thr	His	Trp	Arg	Gln	Asn	Thr	Glu		
			565						570					575			
Lys	Leu	Asp	Lys	Ser	Arg	Ala	Glu	Ile	Glu	His	Glu	Ala	Leu	Ile	Asp		
		580						585					590				
Gly	Asn	Leu	Ala	Thr	Glu	Ala	Asn	Leu	Ile	Ile	Leu	Asp	Thr	Leu	Glu		
	595						600					605					
Ile	Val	Val	Gln	Thr	Val	Ser	Val	Thr	Glu	Ser	Lys	Glu	Ser	Ile	Leu		
610						615					620						
Gly	Gly	Val	Leu	Lys	Val	Leu	Leu	His	Ser	Met	Ala	Cys	Asn	Gln	Ser		
625					630					635					640		
Ala	Val	Tyr	Leu	Gln	His	Cys	Phe	Ala	Thr	Gln	Arg	Ala	Leu	Val	Ser		
			645						650					655			
Lys	Phe	Pro	Glu	Leu	Leu	Phe	Glu	Glu	Glu	Thr	Glu	Gln	Cys	Ala	Asp		
		660					665						670				

Leu Cys Leu Arg Leu Leu Arg His Cys Ser Ser Ser Ile Gly Thr Ile
 675 680 685
 Arg Ser His Pro Ser Ala Ser Leu Tyr Leu Leu Met Arg Gln Asn Phe
 690 695 700
 Glu Ile Gly Asn Asn Phe Ala Arg Val Lys Met Gln Val Pro Met Ser
 705 710 715 720
 Leu Ser Ser Leu Val Gly Thr Ser Gln Asn Phe Asn Glu Glu Phe Leu
 725 730 735
 Arg Arg Ser Leu Lys Thr Ile Leu Thr Tyr Ala Glu Glu Asp Leu Glu
 740 745 750
 Leu Arg Glu Thr Thr Phe Pro Asp Gln Val Gln Asp Leu Val Phe Asn
 755 760 765
 Leu His Met Ile Leu Ser Asp Thr Val Lys Met Lys Glu His Gln Glu
 770 775 780
 Asp Pro Glu Met Leu Ile Asp Leu Met Tyr Arg Ile Ala Lys Gly Tyr
 785 790 795 800
 Gln Thr Ser Pro Asp Leu Arg Leu Thr Trp Leu Gln Asn Met Ala Gly
 805 810 815
 Lys His Ser Glu Arg Ser Asn His Ala Glu Ala Ala Gln Cys Leu Val
 820 825 830
 His Ser Ala Ala Leu Val Ala Glu Tyr Leu Ser Met Leu Glu Asp Arg
 835 840 845
 Lys Tyr Leu Pro Val Gly Cys Val Thr Phe Gln Asn Ile Ser Ser Asn
 850 855 860
 Val Leu Glu Glu Ser Ala Val Ser Asp Asp Val Val Ser Pro Asp Glu
 865 870 875 880
 Glu Gly Ile Cys Ser Gly Lys Tyr Phe Thr Glu Ser Gly Leu Val Gly
 885 890 895
 Leu Leu Glu Gln Ala Ala Ala Ser Phe Ser Met Ala Gly Met Tyr Glu
 900 905 910
 Ala Val Asn Glu Val Tyr Lys Val Leu Ile Pro Ile His Glu Ala Asn
 915 920 925
 Arg Asp Ala Lys Lys Leu Ser Thr Ile His Gly Lys Leu Gln Glu Ala
 930 935 940
 Phe Ser Lys Ile Val His Gln Ser Thr Gly Trp Glu Arg Met Phe Gly
 945 950 955 960
 Thr Tyr Phe Arg Val Gly Phe Tyr Gly Thr Lys Phe Gly Asp Leu Asp
 965 970 975
 Glu Gln Glu Phe Val Tyr Lys Glu Pro Ala Ile Thr Lys Leu Ala Glu
 980 985 990

Ile Ser His Arg Leu Glu Gly Phe Tyr Gly Glu Arg Phe Gly Glu Asp
 995 1000 1005
 Val Val Glu Val Ile Lys Asp Ser Asn Pro Val Asp Lys Cys Lys Leu
 1010 1015 1020
 Asp Pro Asn Lys Ala Tyr Ile Gln Ile Thr Tyr Val Glu Pro Tyr Phe
 1025 1030 1035 1040
 Asp Thr Tyr Glu Met Lys Asp Arg Ile Thr Tyr Phe Asp Lys Asn Tyr
 1045 1050 1055
 Asn Leu Arg Arg Phe Met Tyr Cys Thr Pro Phe Thr Leu Asp Gly Arg
 1060 1065 1070
 Ala His Gly Glu Leu His Glu Gln Phe Lys Arg Lys Thr Ile Leu Thr
 1075 1080 1085
 Thr Ser His Ala Phe Pro Tyr Ile Lys Thr Arg Val Asn Val Thr His
 1090 1095 1100
 Lys Glu Glu Ile Ile Leu Thr Pro Ile Glu Val Ala Ile Glu Asp Met
 1105 1110 1115 1120
 Gln Lys Lys Thr Gln Glu Leu Ala Phe Ala Thr His Gln Asp Pro Ala
 1125 1130 1135
 Asp Pro Lys Met Leu Gln Met Val Leu Gln Gly Ser Val Gly Thr Thr
 1140 1145 1150
 Val Asn Gln Gly Pro Leu Glu Val Ala Gln Val Phe Leu Ser Glu Ile
 1155 1160 1165
 Pro Ser Asp Pro Lys Leu Phe Arg His His Asn Lys Leu Arg Leu Cys
 1170 1175 1180
 Phe Lys Asp Phe Thr Lys Arg Cys Glu Asp Ala Leu Arg Lys Asn Lys
 1185 1190 1195 1200
 Ser Leu Ile Gly Pro Val Gln Lys Glu Tyr Gln Arg Glu Leu Gly Lys
 1205 1210 1215
 Leu Ser Ser Pro
 1220

<210> 15
 <211> 987
 <212> PRT
 <213> Homo sapiens

<220>
 <223> human CLASP-5

<400> 15
 Met Asn Ala Asp Thr Ala Pro Thr Ser Pro Cys Pro Ser Ile Ser Ser
 1 5 10 15
 Gln Asn Ser Ser Ser Cys Ser Ser Phe Gln Asp Gln Lys Ile Ala Ser
 20 25 30

Met Phe Asp Arg Thr Ser Arg Val Pro Ala Ser Ser Thr Ser Ser Pro
 35 40 45
 Gly Leu Leu Phe Thr Glu Leu Ala Ala Ala Leu Asp Ala Glu Gly Glu
 50 55 60
 Gly Ile Ser Glu Val Gln Arg Lys Ala Val Ser Ala Ile His Ser Leu
 65 70 75 80
 Leu Ser Ser His Asp Leu Asp Pro Arg Cys Val Lys Pro Glu Val Lys
 85 90 95
 Val Lys Ile Ala Ala Leu Tyr Leu Pro Leu Val Gly Ile Ile Leu Asp
 100 105 110
 Ala Leu Pro Gln Leu Cys Asp Phe Thr Val Ala Asp Thr Arg Arg Tyr
 115 120 125
 Arg Thr Ser Gly Ser Asp Glu Glu Gln Glu Gly Ala Gly Ala Ile Thr
 130 135 140
 Gln Asn Val Ala Leu Ala Ile Ala Gly Asn Asn Phe Asn Leu Lys Thr
 145 150 155 160
 Ser Gly Ile Val Leu Ser Ser Leu Pro Tyr Lys Gln Tyr Asn Met Leu
 165 170 175
 Asn Ala Asp Thr Thr Arg Asn Leu Met Ile Cys Phe Leu Trp Ile Met
 180 185 190
 Lys Asn Ala Asp Gln Ser Leu Ile Arg Lys Trp Ile Ala Asp Leu Pro
 195 200 205
 Ser Thr Gln Leu Asn Arg Ile Leu Asp Leu Leu Phe Ile Cys Val Leu
 210 215 220
 Cys Phe Glu Tyr Lys Gly Lys Gln Ser Ser Asp Lys Val Ser Thr Gln
 225 230 235 240
 Val Leu Gln Lys Ser Arg Asp Val Lys Ala Arg Leu Glu Glu Ala Leu
 245 250 255
 Leu Arg Gly Glu Gly Ala Arg Gly Glu Met Met Arg Arg Arg Ala Pro
 260 265 270
 Gly Asn Asp Arg Phe Pro Gly Leu Asn Glu Asn Leu Arg Trp Lys Lys
 275 280 285
 Glu Gln Thr His Trp Arg Gln Ala Asn Glu Lys Leu Asp Lys Thr Lys
 290 295 300
 Ala Glu Leu Asp Gln Glu Ala Leu Ile Ser Gly Asn Leu Ala Thr Glu
 305 310 315 320
 Ala His Leu Ile Ile Leu Asp Met Gln Glu Asn Ile Ile Gln Ala Ser
 325 330 335
 Ser Ala Leu Asp Cys Lys Asp Ser Leu Leu Gly Gly Val Leu Arg Val
 340 345 350

Leu Val Asn Ser Leu Asn Cys Asp Gln Ser Thr Thr Tyr Leu Thr His
 355 360 365
 Cys Phe Ala Thr Leu Arg Ala Leu Ile Ala Lys Phe Gly Asp Leu Leu
 370 375 380
 Phe Glu Glu Glu Val Glu Gln Cys Phe Asp Leu Cys His Gln Val Leu
 385 390 395 400
 His His Cys Ser Ser Ser Met Asp Val Thr Arg Ser Gln Ala Cys Ala
 405 410 415
 Thr Leu Tyr Leu Leu Met Arg Phe Ser Phe Gly Ala Thr Ser Asn Phe
 420 425 430
 Ala Arg Val Lys Met Gln Val Thr Met Ser Leu Ala Ser Leu Val Gly
 435 440 445
 Arg Ala Pro Asp Phe Asn Glu Glu His Leu Arg Arg Ser Leu Arg Thr
 450 455 460
 Ile Leu Ala Tyr Ser Glu Glu Asp Thr Ala Met Gln Met Thr Pro Phe
 465 470 475 480
 Pro Thr Gln Val Glu Glu Leu Leu Cys Asn Leu Asn Ser Ile Leu Tyr
 485 490 495
 Asp Thr Val Lys Met Arg Glu Phe Gln Glu Asp Pro Glu Met Leu Met
 500 505 510
 Asp Leu Met Tyr Arg Ile Ala Lys Ser Tyr Gln Ala Ser Pro Asp Leu
 515 520 525
 Arg Leu Thr Trp Leu Gln Asn Met Ala Glu Lys His Thr Lys Lys Lys
 530 535 540
 Cys Tyr Thr Glu Ala Ala Met Cys Leu Val His Ala Ala Ala Leu Val
 545 550 555 560
 Ala Glu Tyr Leu Ser Met Leu Glu Asp His Ser Tyr Leu Pro Val Gly
 565 570 575
 Ser Val Ser Phe Gln Asn Ile Ser Ser Asn Val Leu Glu Glu Ser Val
 580 585 590
 Val Ser Glu Asp Thr Leu Ser Pro Asp Glu Asp Gly Val Cys Ala Gly
 595 600 605
 Gln Tyr Phe Thr Glu Ser Gly Leu Val Gly Leu Leu Glu Gln Ala Ala
 610 615 620
 Glu Leu Phe Ser Thr Gly Gly Leu Tyr Glu Thr Val Asn Glu Val Tyr
 625 630 635 640
 Lys Leu Val Ile Pro Ile Leu Glu Ala His Arg Glu Phe Arg Lys Leu
 645 650 655
 Thr Leu Thr His Ser Lys Leu Gln Arg Ala Phe Asp Ser Ile Val Asn
 660 665 670

Lys Asp His Lys Arg Met Phe Gly Thr Tyr Phe Arg Val Gly Phe Phe
 675 680 685
 Gly Ser Lys Phe Gly Asp Leu Asp Glu Gln Glu Phe Val Tyr Lys Glu
 690 695 700
 Pro Ala Ile Thr Lys Leu Pro Glu Ile Ser His Arg Leu Glu Ala Phe
 705 710 715 720
 Tyr Gly Gln Cys Phe Gly Ala Glu Phe Val Glu Val Ile Lys Asp Ser
 725 730 735
 Thr Pro Val Asp Lys Thr Lys Leu Asp Pro Asn Lys Ala Tyr Ile Gln
 740 745 750
 Ile Thr Phe Val Glu Pro Tyr Phe Asp Glu Tyr Glu Met Lys Asp Arg
 755 760 765
 Val Thr Tyr Phe Glu Lys Asn Phe Asn Leu Arg Arg Phe Met Tyr Thr
 770 775 780
 Thr Pro Phe Thr Leu Glu Gly Arg Pro Arg Gly Glu Leu His Glu Gln
 785 790 795 800
 Tyr Arg Arg Asn Thr Val Leu Thr Thr Met His Ala Phe Pro Tyr Ile
 805 810 815
 Lys Thr Arg Ile Ser Val Ile Gln Lys Glu Glu Phe Val Leu Thr Pro
 820 825 830
 Ile Glu Val Ala Ile Glu Asp Met Lys Lys Lys Thr Leu Gln Leu Ala
 835 840 845
 Val Ala Ile Asn Gln Glu Pro Pro Asp Ala Lys Met Leu Gln Met Val
 850 855 860
 Leu Gln Gly Ser Val Gly Ala Thr Val Asn Gln Gly Pro Leu Glu Val
 865 870 875 880
 Ala Gln Val Phe Leu Ala Glu Ile Pro Ala Asp Pro Lys Leu Tyr Arg
 885 890 895
 His His Asn Lys Leu Arg Leu Cys Phe Lys Glu Phe Ile Met Arg Cys
 900 905 910
 Gly Glu Ala Val Glu Lys Asn Lys Arg Leu Ile Thr Ala Asp Gln Arg
 915 920 925
 Glu Tyr Gln Gln Glu Leu Lys Lys Asn Tyr Asn Lys Leu Lys Glu Asn
 930 935 940
 Leu Arg Pro Met Ile Glu Arg Lys Ile Pro Glu Leu Tyr Lys Pro Ile
 945 950 955 960
 Phe Arg Val Glu Ser Gln Lys Arg Asp Ser Phe His Arg Ser Ser Phe
 965 970 975
 Arg Lys Cys Glu Thr Gln Leu Ser Gln Gly Ser
 980 985

<210> 16
 <211> 24
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:DOCK motifs A
 and B from human CLASP-1

 <400> 16
 Tyr Arg Val Ala Phe Tyr Gly Gln Gly Phe Phe Glu Glu Glu Glu Gly
 1 5 10 15

 Lys Glu Tyr Ile Tyr Lys Glu Pro
 20

<210> 17
 <211> 38
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:DOCK motifs A
 and B from human KIAA1058

 <400> 17
 Phe Arg Val Ala Phe Phe Gly Gln Ala Ala Gln Tyr Gln Phe Thr Asp
 1 5 10 15

 Ser Glu Thr Asp Val Glu Gly Phe Phe Glu Asp Glu Asp Gly Lys Glu
 20 25 30

 Tyr Ile Tyr Lys Glu Pro
 35

<210> 18
 <211> 14
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:DOCK motif B
 from human CLASP-2

 <400> 18
 Phe Glu Asp Glu Asp Gly Lys Glu Tyr Ile Tyr Lys Glu Pro
 1 5 10

<210> 19
 <211> 24
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:DOCK motifs A
 and B from human CLASP-6

<400> 19

Phe Arg Val Ala Phe Phe Gly Gln Gly Phe Phe Glu Asp Glu Asp Gly
1 5 10 15

Lys Glu Tyr Ile Tyr Lys Glu Pro
20

<210> 20

<211> 24

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs A
and B from human CLASP-4

<400> 20

Phe Arg Val Ala Phe Tyr Gly Gln Ser Phe Phe Glu Glu Glu Asp Gly
1 5 10 15

Lys Glu Tyr Ile Tyr Lys Glu Pro
20

<210> 21

<211> 31

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs A
and B from canonical DOCK180

<400> 21

Phe Ala Val Gly Tyr Tyr Gly Gln Gly Phe Pro Thr Phe Leu Arg Gly
1 5 10 15

Lys Val Phe Ile Tyr Arg Gly Lys Glu Tyr Glu Arg Arg Glu Asp
20 25 30

<210> 22

<211> 31

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs A
and B from canonical DOCK2

<400> 22

Phe Ala Val Gly Tyr Tyr Gly Gln Gly Phe Pro Ser Phe Leu Arg Asn
1 5 10 15

Lys Val Phe Ile Tyr Arg Gly Lys Glu Tyr Glu Arg Arg Glu Asp
20 25 30

<210> 23
<211> 24
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs A
and B from canonical DOCK3

<400> 23

Phe Arg Val Gly Phe Tyr Gly Arg Lys Phe Pro Phe Phe Leu Arg Asn
1 5 10 15

Lys Glu Tyr Val Cys Arg Gly His
20

<210> 24
<211> 24
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs A
and B from human KIAA0716

<400> 24

Phe Arg Val Gly Phe Tyr Gly Lys Lys Phe Pro Phe Phe Leu Arg Asn
1 5 10 15

Lys Glu Phe Val Cys Arg Gly His
20

<210> 25
<211> 23
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs A
and B from human CLASP-3

<400> 25

Phe Arg Val Gly Phe Tyr Gly Thr Lys Phe Gly Asp Leu Asp Glu Gln
1 5 10 15

Glu Phe Val Tyr Lys Glu Pro
20

<210> 26
<211> 60
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motif C
from rat TRG

<400> 26

Pro Lys Leu Thr Pro Leu Ser Glu Ile Ser Gln Arg Leu Leu Lys Leu
1 5 10 15
Tyr Ser Asp Lys Phe Gly Ser Glu Asn Val Lys Met Ile Gln Asp Ser
20 25 30
Gly Lys Val Asn Pro Lys Asp Leu Asp Ser Lys Phe Ala Tyr Ile Gln
35 40 45
Val Thr His Val Thr Pro Phe Phe Asp Glu Lys Glu
50 55 60

<210> 27

<211> 60

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motif C
from human CLASP-1

<400> 27

Pro Lys Leu Thr Gly Leu Ser Glu Ile Ser Gln Arg Leu Leu Lys Leu
1 5 10 15
Tyr Ala Asp Lys Phe Gly Ala Asp Asn Val Lys Ile Ile Gln Asp Ser
20 25 30
Asn Lys Val Asn Pro Lys Asp Leu Asp Pro Lys Tyr Ala Tyr Ile Gln
35 40 45
Val Thr Tyr Val Thr Pro Phe Phe Glu Glu Lys Glu
50 55 60

<210> 28

<211> 60

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motif C
from human CLASP-2

<400> 28

Pro Lys Leu Thr Pro Leu Ser Glu Ile Ser Gln Arg Leu Leu Lys Leu
1 5 10 15
Tyr Ser Asp Lys Phe Gly Ser Glu Asn Val Lys Met Thr Gln Asp Ser
20 25 30
Gly Lys Val Asn Pro Lys Asp Leu Asp Ser Lys Tyr Ala Tyr Ile Gln
35 40 45
Val Thr His Val Ile Pro Phe Phe Asp Glu Lys Glu
50 55 60

<210> 29
<211> 60
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motif C
from human CLASP-4

<400> 29

Pro Lys Leu Thr Gly Leu Ser Glu Ile Ser Leu Arg Leu Val Lys Leu
1 5 10 15
Tyr Gly Glu Lys Phe Gly Thr Glu Asn Val Lys Ile Ile Gln Asp Ser
20 25 30
Asp Lys Val Asn Ala Lys Glu Leu Asp Pro Lys Tyr Ala His Ile Gln
35 40 45
Val Thr Tyr Val Lys Pro Tyr Phe Asp Asp Lys Glu
50 55 60

<210> 30
<211> 60
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motif C
from human CLASP-3

<400> 30

Pro Ala Ile Thr Lys Leu Ala Glu Ile Ser His Arg Leu Glu Gly Phe
1 5 10 15
Tyr Gly Glu Arg Phe Gly Glu Asp Val Val Glu Val Ile Lys Asp Ser
20 25 30
Asn Pro Val Asp Lys Cys Lys Leu Asp Pro Asn Lys Ala Tyr Ile Gln
35 40 45
Ile Thr Tyr Val Glu Pro Tyr Phe Asp Thr Tyr Glu
50 55 60

<210> 31
<211> 54
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motif C
from human KIAA0716

<400> 31

His Asp Tyr Glu Arg Leu Glu Ala Phe Gln Gln Arg Met Leu Asn Glu
1 5 10 15
Phe Pro His Ala Ile Ala Met Gln His Ala Asn Gln Pro Asp Glu Thr
20 25 30

Ile Phe Gln Ala Glu Ala Gln Tyr Leu Gln Ile Tyr Ala Val Thr Pro
 35 40 45

Ile Pro Glu Ser Gln Glu
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<210> 32
 <211> 54
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:DOCK motif C
 from canonical DOCK3

<400> 32
 His Asp Tyr Glu Arg Leu Glu Ala Phe Gln Gln Arg Met Leu Ser Glu
 1 5 10 15

Phe Pro Gln Ala Val Ala Met Gln His Pro Asn His Pro Asp Asp Ala
 20 25 30

Ile Leu Gln Cys Asp Ala Gln Tyr Leu Gln Ile Tyr Ala Val Thr Pro
 35 40 45

Ile Pro Asp Tyr Val Asp
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<210> 33
 <211> 46
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:DOCK motif C
 from canonical DOCK2

<400> 33
 Phe Gln Met Gln Leu Met Thr Gln Phe Pro Asn Ala Glu Lys Met Asn
 1 5 10 15

Thr Thr Ser Ala Pro Gly Asp Asp Val Lys Asn Ala Pro Gly Gln Tyr
 20 25 30

Ile Gln Cys Phe Thr Val Gln Pro Val Leu Asp Glu His Pro
 35 40 45

<210> 34
 <211> 53
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:DOCK motif C
 from canonical DOCK180

<400> 34
 Glu Tyr Glu Arg Arg Glu Asp Phe Gln Met Gln Leu Met Thr Gln Phe
 1 5 10 15
 Pro Asn Ala Glu Lys Met Asn Thr Thr Ser Ala Pro Gly Asp Asp Val
 20 25 30
 Lys Asn Ala Pro Gly Gln Tyr Ile Gln Cys Phe Thr Val Gln Pro Val
 35 40 45
 Leu Asp Glu His Pro
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<210> 35
 <211> 45
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:DOCK motifs D
 and E from human CLASP-1

<400> 35
 Arg Thr Ile Leu Thr Thr Ser His Leu Phe Pro Tyr Val Lys Lys Arg
 1 5 10 15
 Ile Gln Val Ile Ser Gln Ser Ser Thr Glu Leu Asn Pro Ile Glu Val
 20 25 30
 Ala Ile Asp Glu Met Ser Arg Lys Val Ser Glu Leu Asn
 35 40 45

<210> 36
 <211> 45
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:DOCK motifs D
 and E from rat TRG

<400> 36
 Arg Thr Ile Leu Thr Ala Ile His Cys Phe Pro Tyr Val Lys Lys Arg
 1 5 10 15
 Ile Pro Val Met Tyr Gln His His Thr Asp Leu Asn Pro Ile Glu Val
 20 25 30
 Ala Ile Asp Glu Met Ser Lys Lys Val Ala Glu Leu His
 35 40 45

<210> 37
 <211> 45
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs D
and E from human KIAA1058

<400> 37

Arg Thr Ile Leu Thr Ala Ile His Cys Phe Pro Tyr Val Lys Lys Arg
1 5 10 15

Ile Pro Val Met Tyr Gln His His Thr Asp Leu Asn Pro Ile Glu Val
20 25 30

Ala Ile Asp Glu Met Ser Lys Lys Val Ala Glu Leu Arg
35 40 45

<210> 38

<211> 45

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs D
and E from human CLASP-2

<400> 38

Arg Thr Ile Leu Thr Ala Ile His Cys Phe Pro Tyr Val Lys Lys Arg
1 5 10 15

Ile Pro Val Met Tyr Gln His His Thr Asp Leu Asn Pro Ile Glu Val
20 25 30

Ala Ile Asp Glu Met Ser Lys Lys Val Ala Glu Leu Arg
35 40 45

<210> 39

<211> 44

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs D
and E from human CLASP-6

<400> 39

Arg Thr Ile Leu Thr Ala Ile His Cys Phe Pro Tyr Val Lys Lys Arg
1 5 10 15

Ile Pro Phe Met Tyr Gln His His Thr Asp Leu Asn Pro Ile Glu Val
20 25 30

His Asp Glu Met Ser Lys Lys Val Ala Glu Leu Arg
35 40

<210> 40

<211> 45

<212> PRT

<213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:DOCK motifs D
 and E from human CLASP-4

<400> 40
 Arg Thr Ile Leu Thr Thr Ser Asn Ser Phe Pro Tyr Val Lys Lys Arg
 1 5 10 15
 Ile Pro Ile Asn Cys Glu Gln Gln Ile Asn Leu Lys Pro Ile Asp Val
 20 25 30
 Ala Thr Asp Glu Ile Lys Asp Lys Thr Ala Glu Leu Gln
 35 40 45

<210> 41
 <211> 45
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:DOCK motifs D
 and E from human CLASP-3

<400> 41
 Lys Thr Ile Leu Thr Thr Ser His Ala Phe Pro Tyr Ile Lys Thr Arg
 1 5 10 15
 Val Asn Val Thr His Lys Glu Glu Ile Ile Leu Thr Pro Ile Glu Val
 20 25 30
 Ala Ile Glu Asp Met Gln Lys Lys Thr Gln Glu Leu Ala
 35 40 45

<210> 42
 <211> 45
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:DOCK motifs D
 and E from human CLASP-5

<400> 42
 Asn Thr Val Leu Thr Thr Met His Ala Phe Pro Tyr Ile Lys Thr Arg
 1 5 10 15
 Ile Ser Val Ile Gln Lys Glu Glu Phe Val Leu Thr Pro Ile Glu Val
 20 25 30
 Ala Ile Glu Asp Met Lys Lys Lys Thr Leu Gln Leu Ala
 35 40 45

<210> 43
 <211> 45
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:DOCK motifs D
 and E from human KIAA0716

<400> 43
 Arg Thr Ser Leu Tyr Leu Val Gln Ser Leu Pro Gly Ile Ser Arg Trp
 1 5 10 15
 Phe Glu Val Glu Lys Arg Glu Val Val Glu Met Ser Pro Leu Glu Asn
 20 25 30
 Ala Ile Glu Val Leu Glu Asn Lys Asn Gln Gln Leu Lys
 35 40 45

<210> 44
 <211> 45
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:DOCK motifs D
 and E from canonical DOCK2

<400> 44
 Arg Thr Ser Phe Val Thr Ala Tyr Lys Leu Pro Gly Ile Leu Arg Trp
 1 5 10 15
 Phe Glu Val Val His Met Ser Gln Thr Thr Ile Ser Pro Leu Glu Asn
 20 25 30
 Ala Ile Glu Thr Met Ser Thr Ala Asn Glu Lys Ile Leu
 35 40 45

<210> 45
 <211> 45
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:DOCK motifs D
 and E from canonical DOCK3

<400> 45
 Arg Thr Thr Leu Thr Leu Thr His Ser Leu Pro Gly Ile Ser Arg Trp
 1 5 10 15
 Phe Glu Val Glu Arg Arg Glu Leu Val Glu Val Ser Pro Leu Glu Asn
 20 25 30
 Ala Ile Gln Val Val Glu Asn Lys Asn Gln Glu Leu Arg
 35 40 45

<210> 46
 <211> 45
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:DOCK motifs D
 and E from canonical DOCK180

<400> 46
 Arg Thr Ser Phe Val Thr Ala Tyr Lys Leu Pro Gly Ile Leu Arg Trp
 1 5 10 15
 Phe Glu Val Val His Met Ser Gln Thr Thr Ile Ser Pro Leu Glu Asn
 20 25 30
 Ala Ile Glu Thr Met Ser Thr Ala Asn Glu Lys Ile Leu
 35 40 45

<210> 47
 <211> 58
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:DOCK motifs F
 and G from human CLASP-1

<400> 47
 Ser Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Lys Val Asn Ala
 1 5 10 15
 Gly Pro Met Ala Tyr Ala Arg Ala Phe Leu Glu Glu Thr Asn Ala Lys
 20 25 30
 Lys Tyr Pro Asp Asn Gln Val Lys Leu Leu Lys Glu Ile Phe Arg Gln
 35 40 45
 Phe Ala Asp Ala Cys Gly Gln Ala Leu Asp
 50 55

<210> 48
 <211> 58
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:DOCK motifs F
 and G from rat TRG

<400> 48
 Lys Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Gln Val Asn Ala
 1 5 10 15
 Gly Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asp Asp Thr Asn Thr Lys
 20 25 30
 Arg Tyr Pro Asp Asn Lys Val Lys Leu Leu Lys Glu Val Phe Arg Gln
 35 40 45
 Phe Val Glu Ala Cys Gly Gln Ala Leu Ala
 50 55

<210> 49
<211> 58
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs F
and G from human KIAA1058

<400> 49

Lys Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Gln Val Asn Ala
1 5 10 15

Gly Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asp Asp Thr Asn Thr Lys
20 25 30

Arg Tyr Pro Asp Asn Lys Val Lys Leu Leu Lys Glu Val Phe Arg Gln
35 40 45

Phe Val Glu Ala Cys Gly Gln Ala Leu Ala
50 55

<210> 50
<211> 58
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs F
and G from human CLASP-2

<400> 50

Lys Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Gln Val Asn Ala
1 5 10 15

Gly Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asp Asp Thr Asn Thr Lys
20 25 30

Arg Tyr Pro Asp Asn Lys Val Lys Leu Leu Lys Glu Val Phe Arg Gln
35 40 45

Phe Val Glu Ala Cys Gly Gln Ala Leu Ala
50 55

<210> 51
<211> 58
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs F
and G from human CLASP-6

<400> 51

Lys Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Gln Val Asn Ala
1 5 10 15

Gly Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asp Asp Thr Asn Thr Lys
20 25 30

Arg Tyr Pro Asp Asn Lys Val Lys Leu Leu Lys Glu Val Phe Arg Gln
35 40 45

Phe Val Glu Ala Cys Gly Gln Ala Leu Ala
50 55

<210> 52

<211> 58

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs F
and G from human CLASP-3

<400> 52

Met Leu Gln Met Val Leu Gln Gly Ser Val Gly Thr Thr Val Asn Gln
1 5 10 15

Gly Pro Leu Glu Val Ala Gln Val Phe Leu Ser Glu Ile Pro Ser Asp
20 25 30

Pro Lys Leu Phe Arg His His Asn Lys Leu Arg Leu Cys Phe Lys Asp
35 40 45

Phe Thr Lys Arg Cys Glu Asp Ala Leu Arg
50 55

<210> 53

<211> 58

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs F
and G from human CLASP-4

<400> 53

Gln Leu Gln Leu Lys Leu Gln Gly Cys Val Ser Val Gln Val Asn Ala
1 5 10 15

Gly Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asn Asp Ser Gln Ala Ser
20 25 30

Lys Tyr Pro Pro Lys Lys Val Ser Glu Leu Lys Asp Met Phe Arg Lys
35 40 45

Phe Ile Gln Ala Cys Ser Ile Ala Leu Glu
50 55

<210> 54

<211> 58

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs F
and G from human CLASP-5

<400> 54

Met Leu Gln Met Val Leu Gln Gly Ser Val Gly Ala Thr Val Asn Gln
1 5 10 15

Gly Pro Leu Glu Val Ala Gln Val Phe Leu Ala Glu Ile Pro Ala Asp
20 25 30

Pro Lys Leu Tyr Arg His His Asn Lys Leu Arg Leu Cys Phe Lys Glu
35 40 45

Phe Ile Met Arg Cys Gly Glu Ala Val Glu
50 55

<210> 55

<211> 60

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs F
and G from human KIAA0716

<400> 55

Pro Leu Thr Met Cys Leu Asn Gly Val Ile Asp Ala Ala Val Asn Gly
1 5 10 15

Gly Val Ser Arg Tyr Gln Glu Ala Phe Phe Val Lys Glu Tyr Ile Leu
20 25 30

Ser His Pro Glu Asp Gly Glu Lys Ile Ala Arg Leu Arg Glu Leu Met
35 40 45

Leu Glu Gln Ala Gln Ile Leu Glu Phe Gly Leu Ala
50 55 60

<210> 56

<211> 60

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs F
and G from canonical DOCK2

<400> 56

Pro Leu Ser Met Leu Leu Asn Gly Ile Val Asp Pro Ala Val Met Gly
1 5 10 15

Gly Phe Ala Lys Tyr Glu Lys Ala Phe Phe Thr Glu Glu Tyr Val Arg
20 25 30

Asp His Pro Glu Asp Gln Asp Lys Leu Thr His Leu Lys Asp Leu Ile
35 40 45

Ala Trp Gln Ile Pro Phe Leu Gly Ala Gly Ile Lys
50 55 60

<210> 57
 <211> 60
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:DOCK motifs F
 and G from canonical DOCK3

 <400> 57
 Leu Leu Ser Met Cys Leu Asn Gly Val Ile Asp Ala Ala Val Asn Gly
 1 5 10 15
 Gly Ile Ala Arg Tyr Gln Glu Ala Phe Phe Asp Lys Asp Tyr Ile Asn
 20 25 30
 Lys His Pro Gly Asp Ala Glu Lys Ile Thr Gln Leu Lys Glu Leu Met
 35 40 45
 Gln Glu Gln Val His Val Leu Gly Val Gly Leu Ala
 50 55 60

<210> 58
 <211> 60
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:DOCK motifs F
 and G from canonical DOCK180

 <400> 58
 Pro Leu Ser Met Leu Leu Asn Gly Ile Val Asp Pro Ala Val Met Gly
 1 5 10 15
 Gly Phe Ala Lys Tyr Glu Lys Ala Phe Phe Thr Glu Glu Tyr Val Arg
 20 25 30
 Asp His Pro Glu Ala His Glu Lys Ile Glu Lys Leu Lys Asp Leu Ile
 35 40 45
 Ala Trp Gln Ile Pro Phe Leu Ala Glu Gly Ile Arg
 50 55 60

<210> 59
 <211> 2149
 <212> DNA
 <213> Homo sapiens

 <220>
 <223> preliminary human CLASP-7 cDNA sequence

 <220>
 <221> CDS
 <222> (2)..(1933)
 <223> human CLASP-7

<400> 59

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Leu	Ser	Glu	Ala	Arg	Glu	Ser	Val	Leu	Gly	Asp	Leu	Leu	Lys	Val	Val		
1					5				10					15			
ctg	tac	agc	ctg	ggc	agt	gcc	cag	agt	gcc	ctc	ttc	ttg	cag	cat	ggc	97	
Leu	Tyr	Ser	Leu	Gly	Ser	Ala	Gln	Ser	Ala	Leu	Phe	Leu	Gln	His	Gly		
			20					25					30				
ctg	gcc	acc	cag	agg	gcc	ctt	gtg	tcc	aag	ttc	ccg	gag	ctg	ctg	ttc	145	
Leu	Ala	Thr	Gln	Arg	Ala	Leu	Val	Ser	Lys	Phe	Pro	Glu	Leu	Leu	Phe		
		35					40					45					
gag	gag	gac	acg	gag	ctg	tgt	gcc	gac	ctg	tgc	ctg	agg	ctc	cta	cga	193	
Glu	Glu	Asp	Thr	Glu	Leu	Cys	Ala	Asp	Leu	Cys	Leu	Arg	Leu	Leu	Arg		
	50					55					60						
cac	tgt	ggc	agc	cgc	atc	agc	acc	atc	cgc	acg	cac	gcc	agc	gcc	tcg	241	
His	Cys	Gly	Ser	Arg	Ile	Ser	Thr	Ile	Arg	Thr	His	Ala	Ser	Ala	Ser		
65					70				75						80		
ctg	tac	ctg	ctc	atg	cga	cag	aac	ttc	gag	atc	ggc	cac	aac	ttt	gcc	289	
Leu	Tyr	Leu	Leu	Met	Arg	Gln	Asn	Phe	Glu	Ile	Gly	His	Asn	Phe	Ala		
				85					90					95			
cgt	gtg	aag	atg	cag	gtc	acc	atg	tct	ctc	tcg	tcc	ctg	gtg	ggg	acg	337	
Arg	Val	Lys	Met	Gln	Val	Thr	Met	Ser	Leu	Ser	Ser	Leu	Val	Gly	Thr		
			100					105					110				
acg	cag	aac	ttc	agt	gaa	gag	cac	ctg	cga	cgt	tca	ctc	aaa	acc	atc	385	
Thr	Gln	Asn	Phe	Ser	Glu	Glu	His	Leu	Arg	Arg	Ser	Leu	Lys	Thr	Ile		
		115					120					125					
ctc	acc	tat	gct	gag	gag	gac	atg	ggg	ctg	cgg	gac	agc	acc	ttc	gca	433	
Leu	Thr	Tyr	Ala	Glu	Glu	Asp	Met	Gly	Leu	Arg	Asp	Ser	Thr	Phe	Ala		
	130					135					140						
gag	cag	gtc	cag	gac	ctg	atg	ttc	aac	ctg	cac	atg	atc	ctg	acg	gac	481	
Glu	Gln	Val	Gln	Asp	Leu	Met	Phe	Asn	Leu	His	Met	Ile	Leu	Thr	Asp		
145					150					155					160		
acg	gtg	aag	atg	aag	gaa	cac	cag	gag	gac	cct	gag	atg	ctc	atc	gac	529	
Thr	Val	Lys	Met	Lys	Glu	His	Gln	Glu	Asp	Pro	Glu	Met	Leu	Ile	Asp		
				165					170					175			
ctc	atg	tac	aga	att	gcc	cgg	ggc	tac	cag	ggc	tca	ccg	gac	ctt	cgg	577	
Leu	Met	Tyr	Arg	Ile	Ala	Arg	Gly	Tyr	Gln	Gly	Ser	Pro	Asp	Leu	Arg		
			180					185					190				
ctg	acc	tgg	ttg	cag	aac	atg	gcc	ggg	aag	cac	gcg	gag	ctg	ggc	aac	625	
Leu	Thr	Trp	Leu	Gln	Asn	Met	Ala	Gly	Lys	His	Ala	Glu	Leu	Gly	Asn		
		195					200					205					
cac	gcc	gag	gcc	gcc	cag	tgc	atg	gtg	cac	gcg	gcc	gcc	ctc	gtg	gct	673	
His	Ala	Glu	Ala	Ala	Gln	Cys	Met	Val	His	Ala	Ala	Ala	Leu	Val	Ala		
	210					215					220						
gag	tac	ctc	gcc	ctg	ctc	gag	gac	cac	cgc	cac	ctg	ccc	gtg	ggc	tgc	721	
Glu	Tyr	Leu	Ala	Leu	Leu	Glu	Asp	His	Arg	His	Leu	Pro	Val	Gly	Cys		
225					230					235					240		

gtt tcc ttc cag aac atc tca tcc aat gtg cta gag gag tcc gcc atc	769
Val Ser Phe Gln Asn Ile Ser Ser Asn Val Leu Glu Glu Ser Ala Ile	
245 250 255	
tcc gac gac atc ctg tcg ccc gac gag gag ggc ttc tgc tcc ggg aag	817
Ser Asp Asp Ile Leu Ser Pro Asp Glu Glu Gly Phe Cys Ser Gly Lys	
260 265 270	
cac ttc act gag ctg ggg ctg gta ggg ttg ctg gaa cag gca gcc ggc	865
His Phe Thr Glu Leu Gly Leu Val Gly Leu Leu Glu Gln Ala Ala Gly	
275 280 285	
tac ttc acc atg ggc ggg ctg tac gag gcg gtg aat gag gtc tac aag	913
Tyr Phe Thr Met Gly Gly Leu Tyr Glu Ala Val Asn Glu Val Tyr Lys	
290 295 300	
aac ctc atc ccc atc ctg gaa gcc cac cgt gac tac aag aag ctg gcc	961
Asn Leu Ile Pro Ile Leu Glu Ala His Arg Asp Tyr Lys Lys Leu Ala	
305 310 315 320	
gcg gtg cac ggc aaa ctg cag gag gcc ttc acc aag atc atg cac cag	1009
Ala Val His Gly Lys Leu Gln Glu Ala Phe Thr Lys Ile Met His Gln	
325 330 335	
agt tcc ggc tgg gag cgc gtg ttc ggg acg tat ttc cgc gtg ggc ttc	1057
Ser Ser Gly Trp Glu Arg Val Phe Gly Thr Tyr Phe Arg Val Gly Phe	
340 345 350	
tac ggc gcc cac ttc ggt gac ctg gat gag cag gag ttt gtg tac aag	1105
Tyr Gly Ala His Phe Gly Asp Leu Asp Glu Gln Glu Phe Val Tyr Lys	
355 360 365	
gag cca tcg atc acg aag ctg gca gag atc tca cac cgg ctg gag gag	1153
Glu Pro Ser Ile Thr Lys Leu Ala Glu Ile Ser His Arg Leu Glu Glu	
370 375 380	
ttc tac acg gag aga ttt ggc gac gac gtc gtt gag att atc aaa gac	1201
Phe Tyr Thr Glu Arg Phe Gly Asp Asp Val Val Glu Ile Ile Lys Asp	
385 390 395 400	
tct tac cct gtg gac aag tcc aag ctt gac tca caa aag gcc tac atc	1249
Ser Tyr Pro Val Asp Lys Ser Lys Leu Asp Ser Gln Lys Ala Tyr Ile	
405 410 415	
cag atc acg tat gtg gaa ccg tac ttt gat acc tac gag ctg aag gac	1297
Gln Ile Thr Tyr Val Glu Pro Tyr Phe Asp Thr Tyr Glu Leu Lys Asp	
420 425 430	
cgg gtg acc tac ttt gac cgc aac tat ggg ctt cgc aca ttc ctg ttc	1345
Arg Val Thr Tyr Phe Asp Arg Asn Tyr Gly Leu Arg Thr Phe Leu Phe	
435 440 445	
tgc acg ccg ttc acg ccg gat ggg cgc gca cac ggg gag ctg ccc gag	1393
Cys Thr Pro Phe Thr Pro Asp Gly Arg Ala His Gly Glu Leu Pro Glu	
450 455 460	
caa cac aag cgt aag acg ctg ctg agc acc gac cac gcc ttc ccc tac	1441
Gln His Lys Arg Lys Thr Leu Leu Ser Thr Asp His Ala Phe Pro Tyr	
465 470 475 480	

atc aag act cgc atc cgt gtg tgc cac cgg gag gag acg gtg ctg acg 1489
 Ile Lys Thr Arg Ile Arg Val Cys His Arg Glu Glu Thr Val Leu Thr
 485 490 495
 cca gtg gag gtg gcc atc gag gac atg cag aag aag aca cgg gag ctg 1537
 Pro Val Glu Val Ala Ile Glu Asp Met Gln Lys Lys Thr Arg Glu Leu
 500 505 510
 gcc ttt gcc acc gag cag gac cca cca gat gct aag atg cta cag atg 1585
 Ala Phe Ala Thr Glu Gln Asp Pro Pro Asp Ala Lys Met Leu Gln Met
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 gtg ctt cag ggc tct gta ggg ccc acc gtg aac cag ggt ccc ctg gag 1633
 Val Leu Gln Gly Ser Val Gly Pro Thr Val Asn Gln Gly Pro Leu Glu
 530 535 540
 gtg gcc cag gtg ttt tta gca gag atc ccg gaa gac ccc aag ctc ttc 1681
 Val Ala Gln Val Phe Leu Ala Glu Ile Pro Glu Asp Pro Lys Leu Phe
 545 550 555 560
 cgg cat cac aac aaa ttg cgg ctc tgc ttc aag gac ttc tgc aag aaa 1729
 Arg His His Asn Lys Leu Arg Leu Cys Phe Lys Asp Phe Cys Lys Lys
 565 570 575
 tgt gag gat gcg ctg cgg aaa aat aag gcc ctg att ggg ccg gac cag 1777
 Cys Glu Asp Ala Leu Arg Lys Asn Lys Ala Leu Ile Gly Pro Asp Gln
 580 585 590
 aag gag tac cac cgt gag ctg gag cgc aac tac tgc cgc ctg cgg gag 1825
 Lys Glu Tyr His Arg Glu Leu Glu Arg Asn Tyr Cys Arg Leu Arg Glu
 595 600 605
 gct ctg cag ccc ctg ctt acc cag cgc ctg ccc cag ctg atg gca ccc 1873
 Ala Leu Gln Pro Leu Leu Thr Gln Arg Leu Pro Gln Leu Met Ala Pro
 610 615 620
 acc cca ccc ggc ctc agg aac tcc ttg aac aga gca agt ttc cga aag 1921
 Thr Pro Pro Gly Leu Arg Asn Ser Leu Asn Arg Ala Ser Phe Arg Lys
 625 630 635 640
 gca gac ctc tga gcccacaagg accaaagctg tacctagagg aaccagcacc 1973
 Ala Asp Leu
 cgggcctcag ctgtctgtgc tgcgagggga gtctgccctg gtgcccactg ggctgtgggg 2033
 tgaccacact gtacttgagg ctggggccctc tgcccctgtg tccccatctg tgtgcaactga 2093
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<210> 60
 <211> 643
 <212> PRT
 <213> Homo sapiens
 <223> preliminary human CLASP-7 cDNA sequence

<400> 60
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Leu Tyr Ser Leu Gly Ser Ala Gln Ser Ala Leu Phe Leu Gln His Gly
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 Leu Ala Thr Gln Arg Ala Leu Val Ser Lys Phe Pro Glu Leu Leu Phe
 35 40 45
 Glu Glu Asp Thr Glu Leu Cys Ala Asp Leu Cys Leu Arg Leu Leu Arg
 50 55 60
 His Cys Gly Ser Arg Ile Ser Thr Ile Arg Thr His Ala Ser Ala Ser
 65 70 75 80
 Leu Tyr Leu Leu Met Arg Gln Asn Phe Glu Ile Gly His Asn Phe Ala
 85 90 95
 Arg Val Lys Met Gln Val Thr Met Ser Leu Ser Ser Leu Val Gly Thr
 100 105 110
 Thr Gln Asn Phe Ser Glu Glu His Leu Arg Arg Ser Leu Lys Thr Ile
 115 120 125
 Leu Thr Tyr Ala Glu Glu Asp Met Gly Leu Arg Asp Ser Thr Phe Ala
 130 135 140
 Glu Gln Val Gln Asp Leu Met Phe Asn Leu His Met Ile Leu Thr Asp
 145 150 155 160
 Thr Val Lys Met Lys Glu His Gln Glu Asp Pro Glu Met Leu Ile Asp
 165 170 175
 Leu Met Tyr Arg Ile Ala Arg Gly Tyr Gln Gly Ser Pro Asp Leu Arg
 180 185 190
 Leu Thr Trp Leu Gln Asn Met Ala Gly Lys His Ala Glu Leu Gly Asn
 195 200 205
 His Ala Glu Ala Ala Gln Cys Met Val His Ala Ala Ala Leu Val Ala
 210 215 220
 Glu Tyr Leu Ala Leu Leu Glu Asp His Arg His Leu Pro Val Gly Cys
 225 230 235 240
 Val Ser Phe Gln Asn Ile Ser Ser Asn Val Leu Glu Glu Ser Ala Ile
 245 250 255
 Ser Asp Asp Ile Leu Ser Pro Asp Glu Glu Gly Phe Cys Ser Gly Lys
 260 265 270
 His Phe Thr Glu Leu Gly Leu Val Gly Leu Leu Glu Gln Ala Ala Gly
 275 280 285
 Tyr Phe Thr Met Gly Gly Leu Tyr Glu Ala Val Asn Glu Val Tyr Lys
 290 295 300
 Asn Leu Ile Pro Ile Leu Glu Ala His Arg Asp Tyr Lys Lys Leu Ala
 305 310 315 320
 Ala Val His Gly Lys Leu Gln Glu Ala Phe Thr Lys Ile Met His Gln
 325 330 335

Ser Ser Gly Trp Glu Arg Val Phe Gly Thr Tyr Phe Arg Val Gly Phe
 340 345 350
 Tyr Gly Ala His Phe Gly Asp Leu Asp Glu Gln Glu Phe Val Tyr Lys
 355 360 365
 Glu Pro Ser Ile Thr Lys Leu Ala Glu Ile Ser His Arg Leu Glu Glu
 370 375 380
 Phe Tyr Thr Glu Arg Phe Gly Asp Asp Val Val Glu Ile Ile Lys Asp
 385 390 395 400
 Ser Tyr Pro Val Asp Lys Ser Lys Leu Asp Ser Gln Lys Ala Tyr Ile
 405 410 415
 Gln Ile Thr Tyr Val Glu Pro Tyr Phe Asp Thr Tyr Glu Leu Lys Asp
 420 425 430
 Arg Val Thr Tyr Phe Asp Arg Asn Tyr Gly Leu Arg Thr Phe Leu Phe
 435 440 445
 Cys Thr Pro Phe Thr Pro Asp Gly Arg Ala His Gly Glu Leu Pro Glu
 450 455 460
 Gln His Lys Arg Lys Thr Leu Leu Ser Thr Asp His Ala Phe Pro Tyr
 465 470 475 480
 Ile Lys Thr Arg Ile Arg Val Cys His Arg Glu Glu Thr Val Leu Thr
 485 490 495
 Pro Val Glu Val Ala Ile Glu Asp Met Gln Lys Lys Thr Arg Glu Leu
 500 505 510
 Ala Phe Ala Thr Glu Gln Asp Pro Pro Asp Ala Lys Met Leu Gln Met
 515 520 525
 Val Leu Gln Gly Ser Val Gly Pro Thr Val Asn Gln Gly Pro Leu Glu
 530 535 540
 Val Ala Gln Val Phe Leu Ala Glu Ile Pro Glu Asp Pro Lys Leu Phe
 545 550 555 560
 Arg His His Asn Lys Leu Arg Leu Cys Phe Lys Asp Phe Cys Lys Lys
 565 570 575
 Cys Glu Asp Ala Leu Arg Lys Asn Lys Ala Leu Ile Gly Pro Asp Gln
 580 585 590
 Lys Glu Tyr His Arg Glu Leu Glu Arg Asn Tyr Cys Arg Leu Arg Glu
 595 600 605
 Ala Leu Gln Pro Leu Leu Thr Gln Arg Leu Pro Gln Leu Met Ala Pro
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 Thr Pro Pro Gly Leu Arg Asn Ser Leu Asn Arg Ala Ser Phe Arg Lys
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 Ala Asp Leu

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tatttggggg gtccgcccc a 141

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agaattccca gctgatgact tggagctgct gctgcagccc cgggaatgcc ggaccacgga 180
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<400> 65

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c                                                    181
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<212> DNA

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gacaccctc gaagcagtgg tgcctctagc atcttcgacc tgaggaacct ggcagctgac 120
tcattgctgc cctctctgct agagcgggag gccccagaag atgtggaccg gcgcaatgaa 180
acccttcgac ggcagcaccg gccccgggcc ctgtcaccct tctaccgggc acctgacgag 240
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<212> DNA

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gagtatactg acatgtctct cttcttagat g                                                    151
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<220>

<223> exon 80380-80500

<400> 68

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ggcccgctct gccatcttct ctgtgacctt cccctcacct gacatcttcc tggatcatcaa 180
ggtgcctgct ggggctgggc aagggggtgg t 211

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<212> DNA
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gccgtgcact tggccaacat cgtgagcagc gctgggcagc tggaccggga ctctgactcg 180
gagggcggtg aggaggcggg gctaacagggc ttggggcggg g 221

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<220>
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tggcttccgt ccagccacgc taactgtcac aaacttcttt aagcaggtgt cctaccctgg 180
ggccaggggac tctcccactc c 201

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<220>
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cttcaagttc ctggctgaca tgaggcgccc gtcgtccctg ctgcggcgac tacgtcctgt 120
gactgggtgcg tggcacaccc catacacaag aagtatcact c 161

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gggcccggccc accaaggaga ttctggagtt ccccgcccg cgaagtctatg cccccatac 180
cagctacagg tacggcctct ggggcccagc tgggcacttg a 221

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gcacagcctc aacttcagca gccgcccagg ctccgtgcgc aaccttgctg tgcgagtgc 120
gtacatgaca ggcgaggacc ccagccaggc tctgccggtc agtggctgtg ccccagggaa 180
ggggggtagg g 191

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<220>
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taccgcgag gccttcacac cgggtggtcta ccataacaag tatgtagggg gacacgtgag 120
gaacttgggg g 131

<210> 77
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<220>
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 tgcacccca ggtacgggggt gggccgggaa ccaagagtcc cgccctgctc c 171

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 cactgtgctg agcgagggca acgtggagca ggagctgcgg gccagtcttg cagcactgcg 180
 cctggccagc cccgaacccc ttgtggcctt ctcccaccac gtgctggaca agctcgtgcg 240
 tctggtcatc agggcccccga tcatcagtgg ccagattggt aagcgaatgt ggccctcagac 300
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<210> 81
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<220>
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 ggatgcccgc ggtcactgcc cacagctggc tgcctacgtc cactacgcct ttgccttcc 180
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 atctgggaga a 251

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 gcgttccaag agcatcagca gcagcaaccc tgacctcgcc gtggccccctg gctctgtgga 180
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 agagatgcag ggtctcaatg tgggaagaaa cctgagggag g 221

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 ggggctttgt cttcagcctg gtccggggcc actacaagca ggtaggagtg ggcgtgggca 180
 ggggtgggcat ggcattggat gaaggcggag c 211

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 acgagcacta cgtgaccctc aacctccccct gctgccccct gtcacctcca gcctcgccct 180
 cccctctgtg gtctccacc acctcccagg tgggctgcct tcacttctgc ctctctctct 240
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 <212> DNA
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<220>
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 cagcacttcc tagctgggct cctgctgacg gagctggcac tggccctcga acctgaggct 180
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 ccgaggccac tgtgaaggct cgtgtggccg agctgtacct gccactgcta tegattgcac 180
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<220>
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 aagctggccg cgggtgcacg caaactgcag gaggccttca ccaagatcat gcaccagggtg 180
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 <223> exon 123290-123510

<400> 102
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 cgtattttccg cgtgggcttc tacggcgccc acttcgggtga cctggatgag caggagtttg 120
 tgtacaagga gccatcgatc acgaagctgg cagagatctc acaccggctg gaggcattgtc 180
 cttgtgggtg ggggtggaac ggggcatggg gctgccttgg g 221

<210> 103
 <211> 124
 <212> DNA
 <213> Homo sapiens

<220>
 <223> exon 123510-123633 (end clone)

<400> 103
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 acacggagag atttggcgac gacgtcgttg agattatcaa agactctaac cctgtggaca 120
 agtc 124

<210> 104
 <211> 1951
 <212> DNA
 <213> Homo sapiens

<220>
 <223> putative human CLASP-7 promoter region

<400> 104
 gggcatgtgg ctcatctcctg taatccccggc actttggggag gccgagggcg gtggatcacc 60
 tgaggtcagg agctccagac cagcctggcc aacatggtga aaccccgctc ctactaaaaa 120
 tacaaaaaat tagccagggtg tgatgggtggg tgcctgtaat cccagctact cgggagggtg 180
 aggcaggaga atcgcttgaa cctgggaggc agaggttgcg gtgagccgag attgtgccat 240
 tgcaactccag tctgggcaac aagagcgaaa tgccacctca aaataaataa ataaataaat 300
 aaataaataa ataaataaat aaataaataa tagaggataa aatgccagca acccatagat 360
 gggaatgaga acagcacgtg caaaggccct gaggcagagc cacggccttg tctgattcaa 420
 cctcaaattc tccctggggc atttgctgac cagggaaaga agggctgtcc aggaggaagg 480
 acctgccggt gcagaggcat gcaggtgaga aaggggtgag ctccctccaga ggggagtgtc 540
 ggctggagaa ttctctaaaa atgctgcagc agtgctggga gagaggccag tggggagaga 600
 tttagagacca tagattaacc aagacatccc cacctcttcc tcttggtaga ggcggccccg 660
 aaagtctaga ctccaaaact ggctcactca ggtcccacca cctggacctg gggcacatct 720
 ccgagcactc cagtgcctag ccaggctcct ctgactcca tgctgtagac tgggagcacg 780
 gacaatgcag gcgctggaga cccctgtgag tcacactgag caagcacccg aacacctctg 840
 tgctcagtt tactcatctg taaaaggagg aaaacaataa tttcttctgc atgtgtgaat 900
 tgcagggccca ggctcaatga catcttagca attagacttt ttgagacagg gtctcgctct 960
 gtcacccagg ctggattgaa atggcacaat cacagctcac tgcagccttg acctccagg 1020
 ctcaagcgat cctcctccct cagactccca agtagctgag attacaggca cacaccacca 1080
 tgcttggtta atttttgcat tttttgtgga cacgggggtct cattatgttg cccaggctgg 1140
 tctccaactc ctgggctcaa acaatcctcc tgcttgggc cccacagtgt ctgggattac 1200
 aggcattgag caccatgcac ggccacgatt atacttacag gtatgattat tagatacatg 1260
 aacatcggtt ttgttttcca gccaggagtc agagggcaga aagagcgccc cccaaacccc 1320
 ggaaatctgg ggcctaccca gcctgggtcc cagcgccctc cctccctccc tccctcctga 1380

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gcttcagttt cccagccct gctcctgggg tggttaagacc acccactaa acccgggag 1440
cctgggggtcc acctagcccc ggtctcagcg cctcccttcc ctccctccct cctcaggctc 1500
agttttctcca gccagctcc caggggtggaa agagcgcccc cgccagctcg ggagtctggg 1560
gcacccccag tctgggtccc agcgctcct ctccctaact tccctcctca gcctcagttt 1620
ccccagccct tctcctaggg tagaaagagc gtccccccag cccgggagtc tggggcccg 1680
ccagcctgga tcccggggcc tctctccgt cccagcctc agtttcccca gccccagga 1740
ctccaggcga cccctccggc ctgcaggggc agcacggagc ggccccgggcc acccggaagg 1800
gccccgcccc cgcgccggcc ccgccccgcc ccggctgccc agaaccggga ggcgcgcgcg 1860
gcggcggggc cggggcccg ggcgcgcgcg gcgggacgcg aggaccatgg ctgcctccga 1920
gcgccgcgcc ttcgcgcaca agatcaacag g 1951

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<210> 105
<211> 2008
<212> PRT
<213> Homo sapiens

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<220>
<223> human CLASP-4

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Arg Thr Val Gln Ser Thr Val Pro Glu Asp Ala Glu Lys Arg Ala Gln
      20             25             30

Ser Leu Phe Val Lys Glu Cys Ile Lys Thr Tyr Ser Thr Asp Trp His
      35             40             45

Val Val Asn Tyr Lys Tyr Glu Asp Phe Ser Gly Asp Phe Arg Met Leu
      50             55             60

Pro Cys Lys Ser Leu Arg Pro Glu Lys Ile Pro Asn His Val Phe Glu
      65             70             75             80

Ile Asp Glu Asp Cys Glu Lys Asp Glu Asp Ser Ser Ser Leu Cys Ser
      85             90             95

Gln Lys Gly Gly Val Ile Lys Gln Gly Trp Leu His Lys Ala Asn Val
      100            105            110

Asn Ser Thr Ile Thr Val Thr Met Lys Val Phe Lys Arg Arg Tyr Phe
      115            120            125

Tyr Leu Thr Gln Leu Pro Asp Gly Ser Tyr Ile Leu Asn Ser Tyr Lys
      130            135            140

Asp Glu Lys Asn Ser Lys Glu Ser Lys Gly Cys Ile Tyr Leu Asp Ala
      145            150            155            160

Cys Ile Asp Val Val Gln Cys Pro Lys Met Arg Arg His Ala Phe Glu
      165            170            175

Leu Lys Met Leu Asp Lys Tyr Ser His Tyr Leu Ala Ala Glu Thr Glu
      180            185            190

Gln Glu Met Glu Glu Trp Leu Ile Thr Leu Lys Lys Ile Ile Gln Ile
      195            200            205

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Asn Thr Asp Ser Leu Val Gln Glu Lys Lys Glu Thr Val Glu Thr Ala
 210 215 220
 Gln Asp Asp Glu Thr Ser Ser Gln Gly Lys Ala Glu Asn Ile Met Ala
 225 230 235 240
 Ser Leu Glu Arg Ser Met His Pro Glu Leu Met Lys Tyr Gly Arg Glu
 245 250 255
 Thr Glu Gln Leu Asn Lys Leu Ser Arg Gly Asp Gly Arg Gln Asn Leu
 260 265 270
 Phe Ser Phe Asp Ser Glu Val Gln Arg Leu Asp Phe Ser Gly Ile Glu
 275 280 285
 Pro Asp Ile Lys Pro Phe Glu Glu Lys Cys Asn Lys Arg Phe Leu Val
 290 295 300
 Asn Cys His Asp Leu Thr Phe Asn Ile Leu Gly Gln Ile Gly Asp Asn
 305 310 315 320
 Ala Lys Gly Pro Pro Thr Asn Val Glu Pro Phe Phe Ile Asn Leu Ala
 325 330 335
 Leu Phe Asp Val Lys Asn Asn Cys Lys Ile Ser Ala Asp Phe His Val
 340 345 350
 Asp Leu Asn Pro Pro Ser Val Arg Glu Met Leu Trp Gly Ser Ser Thr
 355 360 365
 Gln Leu Ala Ser Asp Gly Ser Pro Lys Gly Ser Ser Pro Glu Ser Tyr
 370 375 380
 Ile His Gly Ile Ala Glu Ser Gln Leu Arg Tyr Ile Gln Gln Gly Ile
 385 390 395 400
 Phe Ser Val Thr Asn Pro His Pro Glu Ile Phe Leu Val Ala Arg Ile
 405 410 415
 Glu Lys Val Leu Gln Gly Asn Ile Thr His Cys Ala Glu Pro Tyr Ile
 420 425 430
 Lys Asn Ser Asp Pro Val Lys Thr Ala Gln Lys Val His Arg Thr Ala
 435 440 445
 Lys Gln Val Cys Ser Arg Leu Gly Gln Tyr Arg Met Pro Phe Ala Trp
 450 455 460
 Ala Ala Arg Pro Ile Phe Lys Asp Thr Gln Gly Ser Leu Asp Leu Asp
 465 470 475 480
 Gly Arg Phe Ser Pro Leu Tyr Lys Gln Asp Ser Ser Lys Leu Ser Ser
 485 490 495
 Glu Asp Ile Leu Lys Leu Leu Ser Glu Tyr Lys Lys Pro Glu Lys Thr
 500 505 510
 Lys Leu Gln Ile Ile Pro Gly Gln Leu Asn Ile Thr Val Glu Cys Val
 515 520 525

Pro Val Asp Leu Ser Asn Cys Ile Thr Ser Ser Tyr Val Pro Leu Lys
 530 535 540
 Pro Phe Glu Lys Asn Cys Gln Asn Ile Thr Val Glu Val Glu Glu Phe
 545 550 555 560
 Val Pro Glu Met Thr Lys Tyr Cys Tyr Pro Phe Thr Ile Tyr Lys Asn
 565 570 575
 His Leu Tyr Val Tyr Pro Leu Gln Leu Lys Tyr Asp Ser Gln Lys Thr
 580 585 590
 Phe Ala Lys Ala Arg Asn Ile Ala Val Cys Val Glu Phe Arg Asp Ser
 595 600 605
 Asp Glu Ser Asp Ala Ser Ala Leu Lys Cys Ile Tyr Gly Lys Pro Ala
 610 615 620
 Gly Ser Val Phe Thr Thr Asn Ala Tyr Ala Val Val Ser His His Asn
 625 630 635 640
 Gln Asn Pro Glu Phe Tyr Asp Glu Ile Lys Ile Glu Leu Pro Ile His
 645 650 655
 Leu His Gln Lys His His Leu Leu Phe Thr Phe Tyr His Val Ser Cys
 660 665 670
 Glu Ile Asn Thr Lys Gly Thr Thr Lys Lys Gln Asp Thr Val Glu Thr
 675 680 685
 Pro Val Gly Phe Ala Trp Val Pro Leu Leu Lys Asp Gly Arg Ile Ile
 690 695 700
 Thr Phe Glu Gln Gln Leu Pro Val Ser Ala Asn Leu Pro Pro Gly Tyr
 705 710 715 720
 Leu Asn Leu Asn Asp Ala Glu Ser Arg Arg Gln Cys Asn Val Asp Ile
 725 730 735
 Lys Trp Val Asp Gly Ala Lys Pro Leu Leu Lys Phe Lys Ser His Leu
 740 745 750
 Glu Ser Thr Ile Tyr Thr Gln Asp Leu His Val His Lys Phe Phe His
 755 760 765
 His Cys Gln Leu Ile Gln Ser Gly Ser Lys Glu Val Pro Gly Glu Leu
 770 775 780
 Ile Lys Tyr Leu Lys Cys Leu His Ala Met Glu Ile Gln Val Met Ile
 785 790 795 800
 Gln Phe Leu Pro Val Ile Leu Met Gln Leu Phe Arg Val Leu Thr Asn
 805 810 815
 Met Thr His Glu Asp Asp Val Pro Ile Asn Cys Thr Met Val Leu Leu
 820 825 830
 His Ile Val Ser Lys Cys His Glu Glu Gly Leu Asp Ser Tyr Leu Arg
 835 840 845

Ser Phe Ile Lys Tyr Ser Phe Arg Pro Glu Lys Pro Ser Ala Pro Gln
 850 855 860
 Ala Gln Leu Ile His Glu Thr Leu Ala Thr Thr Met Ile Ala Ile Leu
 865 870 875 880
 Lys Gln Ser Ala Asp Phe Leu Ser Ile Asn Lys Leu Leu Lys Tyr Ser
 885 890 895
 Trp Phe Phe Phe Glu Ile Ile Ala Lys Ser Met Ala Thr Tyr Leu Leu
 900 905 910
 Glu Glu Asn Lys Ile Lys Leu Pro Arg Gly Gln Arg Phe Pro Glu Thr
 915 920 925
 Tyr His His Val Leu His Ser Leu Leu Leu Ala Ile Ile Pro His Val
 930 935 940
 Thr Ile Arg Tyr Ala Glu Ile Pro Asp Glu Ser Arg Asn Val Asn Tyr
 945 950 955 960
 Ser Leu Ala Ser Phe Leu Lys Arg Cys Leu Thr Leu Met Asp Arg Gly
 965 970 975
 Phe Ile Phe Asn Leu Ile Asn Asp Tyr Ile Ser Gly Phe Ser Pro Lys
 980 985 990
 Asp Pro Lys Val Leu Ala Glu Tyr Lys Phe Glu Phe Leu Gln Thr Ile
 995 1000 1005
 Cys Asn His Glu His Tyr Ile Pro Leu Asn Leu Pro Met Ala Phe Ala
 1010 1015 1020
 Lys Pro Lys Leu Gln Arg Val Gln Asp Ser Asn Leu Glu Tyr Ser Leu
 1025 1030 1035 1040
 Ser Asp Glu Tyr Cys Lys His His Phe Leu Val Gly Leu Leu Leu Arg
 1045 1050 1055
 Glu Thr Ser Ile Ala Leu Gln Asp Asn Tyr Glu Ile Arg Tyr Thr Ala
 1060 1065 1070
 Ile Ser Val Ile Lys Asn Leu Leu Ile Lys His Ala Phe Asp Thr Arg
 1075 1080 1085
 Tyr Gln His Lys Asn Gln Gln Ala Lys Ile Ala Gln Leu Tyr Leu Pro
 1090 1095 1100
 Phe Val Gly Leu Leu Leu Glu Asn Ile Gln Arg Leu Ala Gly Arg Asp
 1105 1110 1115 1120
 Thr Leu Tyr Ser Cys Ala Ala Met Pro Asn Ser Ala Ser Arg Asp Glu
 1125 1130 1135
 Phe Pro Cys Gly Phe Thr Ser Pro Ala Asn Arg Gly Ser Leu Ser Thr
 1140 1145 1150
 Asp Lys Asp Thr Ala Tyr Gly Ser Phe Gln Asn Gly His Gly Ile Lys
 1155 1160 1165

Arg Glu Asp Ser Arg Gly Ser Leu Ile Pro Glu Gly Ala Thr Gly Phe
 1170 1175 1180
 Pro Asp Gln Gly Asn Thr Gly Glu Asn Thr Arg Gln Ser Ser Thr Arg
 1185 1190 1195 1200
 Ser Ser Val Ser Gln Tyr Asn Arg Leu Asp Gln Tyr Glu Ile Arg Ser
 1205 1210 1215
 Leu Leu Met Cys Tyr Leu Tyr Ile Val Lys Met Ile Ser Glu Asp Thr
 1220 1225 1230
 Leu Leu Thr Tyr Trp Asn Lys Val Ser Pro Gln Glu Leu Ile Asn Ile
 1235 1240 1245
 Leu Ile Leu Leu Glu Val Cys Leu Phe His Phe Arg Tyr Met Gly Lys
 1250 1255 1260
 Arg Asn Ile Ala Arg Val His Asp Ala Trp Leu Ser Lys His Phe Gly
 1265 1270 1275 1280
 Ile Asp Arg Lys Ser Gln Thr Met Pro Ala Leu Arg Asn Arg Ser Gly
 1285 1290 1295
 Val Met Gln Ala Arg Leu Gln His Leu Ser Ser Leu Glu Ser Ser Phe
 1300 1305 1310
 Thr Leu Asn His Ser Ser Thr Thr Thr Glu Ala Asp Ile Phe His Gln
 1315 1320 1325
 Ala Leu Leu Glu Gly Asn Thr Ala Thr Glu Val Ser Leu Thr Val Leu
 1330 1335 1340
 Asp Thr Ile Ser Phe Phe Thr Gln Cys Phe Lys Thr Gln Leu Leu Asn
 1345 1350 1355 1360
 Asn Asp Gly His Asn Pro Leu Met Lys Lys Val Phe Asp Ile His Leu
 1365 1370 1375
 Ala Phe Leu Lys Asn Gly Gln Ser Glu Val Ser Leu Lys His Val Phe
 1380 1385 1390
 Ala Ser Leu Arg Ala Phe Ile Ser Lys Phe Pro Ser Ala Phe Phe Lys
 1395 1400 1405
 Gly Arg Val Asn Met Cys Ala Ala Phe Cys Tyr Glu Val Leu Lys Cys
 1410 1415 1420
 Cys Thr Ser Lys Ile Ser Ser Thr Arg Asn Glu Ala Ser Ala Leu Leu
 1425 1430 1435 1440
 Tyr Leu Leu Met Arg Asn Asn Phe Glu Tyr Thr Lys Arg Lys Thr Phe
 1445 1450 1455
 Leu Arg Thr His Leu Gln Ile Ile Ile Ala Val Ser Gln Leu Ile Ala
 1460 1465 1470
 Asp Val Ala Leu Ser Gly Gly Ser Arg Phe Gln Glu Ser Leu Phe Ile
 1475 1480 1485

Ile Asn Asn Phe Ala Asn Ser Asp Arg Pro Met Lys Ala Thr Ala Phe
 1490 1495 1500
 Pro Ala Glu Val Lys Asp Leu Thr Lys Arg Ile Arg Thr Val Leu Met
 1505 1510 1515 1520
 Ala Thr Ala Gln Met Lys Glu His Glu Lys Asp Pro Glu Met Leu Ile
 1525 1530 1535
 Asp Leu Gln Tyr Ser Leu Ala Lys Ser Tyr Ala Ser Thr Pro Glu Leu
 1540 1545 1550
 Arg Lys Thr Trp Leu Asp Ser Met Ala Lys Ile His Val Lys Asn Gly
 1555 1560 1565
 Asp Phe Ser Glu Ala Ala Met Cys Tyr Val His Val Ala Ala Leu Val
 1570 1575 1580
 Ala Glu Phe Leu His Arg Lys Lys Leu Phe Pro Asn Gly Cys Ser Ala
 1585 1590 1595 1600
 Phe Lys Lys Ile Thr Pro Asn Ile Asp Glu Glu Gly Ala Met Lys Glu
 1605 1610 1615
 Asp Ala Gly Met Met Asp Val His Tyr Ser Glu Glu Val Leu Leu Glu
 1620 1625 1630
 Leu Leu Glu Gln Cys Val Asp Gly Leu Trp Lys Ala Glu Arg Tyr Glu
 1635 1640 1645
 Ile Ile Ser Glu Ile Ser Lys Leu Ile Val Pro Ile Tyr Glu Lys Arg
 1650 1655 1660
 Arg Glu Phe Glu Lys Leu Thr Gln Val Tyr Arg Thr Leu His Gly Ala
 1665 1670 1675 1680
 Tyr Thr Lys Ile Leu Glu Val Met His Thr Lys Lys Arg Leu Leu Gly
 1685 1690 1695
 Thr Phe Phe Arg Val Ala Phe Tyr Gly Gln Ser Phe Phe Glu Glu Glu
 1700 1705 1710
 Asp Gly Lys Glu Tyr Ile Tyr Lys Glu Pro Lys Leu Thr Gly Leu Ser
 1715 1720 1725
 Glu Ile Ser Leu Arg Leu Val Lys Leu Tyr Gly Glu Lys Phe Gly Thr
 1730 1735 1740
 Glu Asn Val Lys Ile Ile Gln Asp Ser Asp Lys Val Asn Ala Lys Glu
 1745 1750 1755 1760
 Leu Asp Pro Lys Tyr Ala His Ile Gln Val Thr Tyr Val Lys Pro Tyr
 1765 1770 1775
 Phe Asp Asp Lys Glu Leu Thr Glu Arg Lys Thr Glu Phe Glu Arg Asn
 1780 1785 1790
 His Asn Ile Ser Arg Phe Val Phe Glu Ala Pro Tyr Thr Leu Ser Gly
 1795 1800 1805

Lys Lys Gln Gly Cys Ile Glu Glu Gln Cys Lys Arg Arg Thr Ile Leu
 1810 1815 1820
 Thr Thr Ser Asn Ser Phe Pro Tyr Val Lys Lys Arg Ile Pro Ile Asn
 1825 1830 1835 1840
 Cys Glu Gln Gln Ile Asn Leu Lys Pro Ile Asp Gly Ala Thr Asp Glu
 1845 1850 1855
 Ile Lys Asp Lys Thr Ala Glu Leu Gln Lys Leu Cys Ser Ser Thr Asp
 1860 1865 1870
 Val Asp Met Ile Gln Leu Gln Leu Lys Leu Gln Gly Trp Val Ser Val
 1875 1880 1885
 Gln Val Asn Ala Gly Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asn Asp
 1890 1895 1900
 Ser Gln Ala Ser Lys Tyr Pro Pro Lys Lys Val Ser Glu Leu Lys Asp
 1905 1910 1915 1920
 Met Phe Arg Lys Phe Ile Gln Ala Cys Ser Ile Ala Leu Glu Leu Asn
 1925 1930 1935
 Glu Arg Leu Ile Lys Glu Asp Gln Val Glu Tyr His Glu Gly Leu Lys
 1940 1945 1950
 Ser Asn Phe Arg Asp Met Val Lys Glu Leu Ser Asp Ile Ile His Glu
 1955 1960 1965
 Gln Ile Leu Gln Glu Asp Thr Met His Ser Pro Trp Met Ser Asn Thr
 1970 1975 1980
 Leu His Val Phe Cys Ala Ile Ser Gly Thr Ser Ser Asp Arg Gly Tyr
 1985 1990 1995 2000
 Gly Ser Pro Arg Tyr Ala Glu Val
 2005

<210> 106
 <211> 2015
 <212> PRT
 <213> Homo sapiens

<220>
 <223> human CLASP-5

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 Arg Thr Leu Gln Pro Ser Leu Pro Glu Glu Gly Val Glu Leu Asp Pro
 35 40 45
 His Val Arg Asp Cys Val Gln Thr Tyr Ile Arg Glu Trp Leu Ile Val
 50 55 60

Asn	Arg	Lys	Asn	Gln	Gly	Ser	Pro	Glu	Ile	Cys	Gly	Phe	Lys	Lys	Thr	65	70	75	80
Gly	Ser	Arg	Lys	Asp	Phe	His	Lys	Thr	Leu	Pro	Lys	Gln	Thr	Phe	Glu	85	90	95	
Ser	Glu	Thr	Leu	Glu	Cys	Ser	Glu	Pro	Ala	Ala	Gln	Ala	Gly	Pro	Arg	100	105	110	
His	Leu	Asn	Val	Leu	Cys	Asp	Val	Ser	Gly	Lys	Gly	Pro	Val	Thr	Ala	115	120	125	
Cys	Asp	Phe	Asp	Leu	Arg	Ser	Leu	Gln	Pro	Asp	Lys	Arg	Leu	Glu	Asn	130	135	140	
Leu	Leu	Gln	Gln	Val	Ser	Ala	Glu	Asp	Phe	Glu	Lys	Gln	Asn	Glu	Glu	145	150	155	160
Ala	Arg	Arg	Thr	Asn	Arg	Gln	Ala	Glu	Leu	Phe	Ala	Leu	Tyr	Pro	Ser	165	170	175	
Val	Asp	Glu	Glu	Asp	Ala	Val	Glu	Ile	Arg	Pro	Val	Pro	Glu	Cys	Pro	180	185	190	
Lys	Glu	His	Leu	Gly	Asn	Arg	Ile	Leu	Val	Lys	Leu	Leu	Thr	Leu	Lys	195	200	205	
Phe	Glu	Ile	Glu	Ile	Glu	Pro	Leu	Phe	Ala	Ser	Ile	Ala	Leu	Tyr	Asp	210	215	220	
Val	Lys	Glu	Arg	Lys	Lys	Ile	Ser	Glu	Asn	Phe	His	Cys	Asp	Leu	Asn	225	230	235	240
Ser	Asp	Gln	Phe	Lys	Gly	Phe	Leu	Arg	Ala	His	Thr	Pro	Ser	Val	Ala	245	250	255	
Ala	Ser	Ser	Gln	Ala	Arg	Ser	Ala	Val	Phe	Ser	Val	Thr	Tyr	Pro	Ser	260	265	270	
Ser	Asp	Ile	Tyr	Leu	Val	Val	Lys	Ile	Glu	Lys	Val	Leu	Gln	Gln	Gly	275	280	285	
Asp	Ile	Gly	Asp	Cys	Ala	Glu	Pro	Tyr	Thr	Val	Ile	Lys	Glu	Ser	Asp	290	295	300	
Gly	Gly	Lys	Ser	Lys	Glu	Lys	Ile	Glu	Lys	Leu	Lys	Leu	Gln	Ala	Glu	305	310	315	320
Ser	Phe	Cys	Gln	Arg	Leu	Gly	Lys	Tyr	Arg	Met	Pro	Phe	Ala	Trp	Ala	325	330	335	
Pro	Ile	Ser	Leu	Ser	Ser	Phe	Phe	Asn	Val	Ser	Thr	Leu	Glu	Arg	Glu	340	345	350	
Val	Thr	Asp	Val	Asp	Ser	Val	Val	Gly	Arg	Ser	Pro	Val	Gly	Glu	Arg	355	360	365	
Arg	Thr	Leu	Ala	Gln	Ser	Arg	Arg	Leu	Ser	Glu	Arg	Ala	Leu	Ser	Leu	370	375	380	

Glu	Glu	Asn	Gly	Val	Gly	Ser	Asn	Phe	Lys	Thr	Ser	Thr	Leu	Ser	Val	385	390	395	400
Ser	Ser	Phe	Phe	Lys	Gln	Glu	Gly	Asp	Arg	Leu	Ser	Asp	Glu	Asp	Leu	405	410	415	
Phe	Lys	Phe	Leu	Ala	Asp	Tyr	Lys	Arg	Ser	Ser	Ser	Leu	Gln	Arg	Arg	420	425	430	
Val	Lys	Ser	Ile	Pro	Gly	Leu	Leu	Arg	Leu	Glu	Ile	Ser	Thr	Ala	Pro	435	440	445	
Glu	Ile	Ile	Asn	Cys	Cys	Leu	Thr	Pro	Glu	Met	Leu	Pro	Val	Lys	Pro	450	455	460	
Phe	Pro	Glu	Asn	Arg	Thr	Arg	Pro	His	Lys	Glu	Ile	Leu	Glu	Phe	Pro	465	470	475	480
Thr	Arg	Glu	Val	Tyr	Val	Pro	His	Thr	Val	Tyr	Arg	Asn	Leu	Leu	Tyr	485	490	495	
Val	Tyr	Pro	Gln	Arg	Leu	Asn	Phe	Val	Asn	Lys	Leu	Ala	Ser	Ala	Arg	500	505	510	
Asn	Ile	Thr	Ile	Lys	Ile	Gln	Phe	Met	Cys	Gly	Glu	Asp	Ala	Ser	Asn	515	520	525	
Ala	Met	Pro	Val	Ile	Phe	Gly	Lys	Ser	Ser	Gly	Pro	Glu	Phe	Leu	Gln	530	535	540	
Glu	Val	Tyr	Thr	Ala	Val	Thr	Tyr	His	Asn	Lys	Ser	Pro	Asp	Phe	Tyr	545	550	555	560
Glu	Glu	Val	Lys	Ile	Lys	Leu	Pro	Ala	Lys	Leu	Thr	Val	Asn	His	His	565	570	575	
Leu	Leu	Phe	Thr	Phe	Tyr	His	Ile	Ser	Cys	Gln	Gln	Lys	Gln	Gly	Ala	580	585	590	
Ser	Val	Glu	Thr	Leu	Leu	Gly	Tyr	Ser	Trp	Leu	Pro	Ile	Leu	Leu	Asn	595	600	605	
Glu	Arg	Leu	Gln	Thr	Gly	Ser	Tyr	Cys	Leu	Pro	Val	Ala	Leu	Glu	Lys	610	615	620	
Leu	Pro	Pro	Asn	Tyr	Ser	Met	His	Ser	Ala	Glu	Lys	Val	Pro	Leu	Gln	625	630	635	640
Asn	Pro	Pro	Ile	Lys	Trp	Ala	Glu	Gly	His	Lys	Gly	Val	Phe	Asn	Ile	645	650	655	
Glu	Val	Gln	Ala	Val	Ser	Ser	Val	His	Thr	Gln	Asp	Asn	His	Leu	Glu	660	665	670	
Lys	Phe	Phe	Thr	Leu	Cys	His	Ser	Leu	Glu	Ser	Gln	Val	Thr	Phe	Pro	675	680	685	
Ile	Arg	Val	Leu	Asp	Gln	Lys	Ile	Ser	Glu	Met	Ala	Leu	Glu	His	Glu	690	695	700	

Leu Lys Leu Ser Ile Ile Cys Leu Asn Ser Ser Arg Leu Glu Pro Leu
 705 710 715 720
 Val Leu Phe Leu His Leu Val Leu Asp Lys Leu Phe Gln Leu Ser Val
 725 730 735
 Gln Pro Met Val Ile Ala Gly Gln Thr Ala Asn Phe Ser Gln Phe Ala
 740 745 750
 Phe Glu Ser Val Val Ala Ile Ala Asn Ser Leu His Asn Ser Lys Asp
 755 760 765
 Leu Ser Lys Asp Gln His Gly Arg Asn Cys Leu Leu Ala Ser Tyr Val
 770 775 780
 His Tyr Val Phe Arg Leu Pro Glu Val Gln Arg Asp Val Pro Lys Ser
 785 790 795 800
 Gly Ala Pro Thr Ala Leu Leu Asp Pro Arg Ser Tyr His Thr Tyr Gly
 805 810 815
 Arg Thr Ser Ala Ala Ala Val Ser Ser Lys Leu Leu Gln Ala Arg Val
 820 825 830
 Met Ser Ser Ser Asn Pro Asp Leu Ala Gly Thr His Ser Ala Ala Asp
 835 840 845
 Glu Glu Val Lys Asn Ile Met Ser Ser Lys Ile Ala Asp Arg Asn Cys
 850 855 860
 Ser Arg Met Ser Tyr Tyr Cys Ser Gly Ser Ser Asp Ala Pro Ser Ser
 865 870 875 880
 Pro Ala Ala Pro Arg Pro Ala Ser Lys Lys His Phe His Glu Glu Leu
 885 890 895
 Ala Leu Gln Met Val Val Ser Thr Gly Met Val Lys Ser Met Ala Gln
 900 905 910
 His Val His Asn Met Asp Lys Arg Asp Ser Phe Arg Arg Thr Arg Phe
 915 920 925
 Ser Asp Arg Phe Met Asp Asp Ile Thr Thr Ile Val Asn Val Val Thr
 930 935 940
 Ser Glu Ile Ala Ala Leu Leu Val Lys Pro Gln Lys Glu Asn Glu Gln
 945 950 955 960
 Ala Glu Lys Met Asn Ile Ser Leu Ala Phe Phe Leu Tyr Asp Leu Leu
 965 970 975
 Ser Leu Met Asp Arg Gly Phe Val Phe Asn Leu Ile Arg His Tyr Cys
 980 985 990
 Ser Gln Leu Ser Ala Lys Leu Ser Asn Leu Pro Thr Leu Ile Ser Met
 995 1000 1005
 Arg Leu Glu Phe Leu Arg Ile Leu Cys Ser His Glu His Tyr Leu Asn
 1010 1015 1020

Leu Asn Leu Phe Phe Met Asn Ala Asp Thr Ala Pro Thr Ser Pro Cys
 1025 1030 1035 1040
 Pro Ser Ile Ser Ser Gln Asn Ser Ser Ser Cys Ser Ser Phe Gln Asp
 1045 1050 1055
 Gln Lys Ile Ala Ser Met Phe Asp Leu Thr Ser Glu Tyr Arg Gln Gln
 1060 1065 1070
 His Phe Leu Thr Gly Leu Leu Phe Thr Glu Leu Ala Ala Ala Leu Asp
 1075 1080 1085
 Ala Glu Gly Glu Gly Ile Ser Lys Val Gln Arg Lys Ala Val Ser Ala
 1090 1095 1100
 Ile His Ser Leu Leu Ser Ser His Asp Leu Asp Pro Arg Cys Val Lys
 1105 1110 1115 1120
 Pro Glu Val Lys Val Lys Ile Ala Ala Leu Tyr Leu Pro Leu Val Gly
 1125 1130 1135
 Ile Ile Leu Asp Ala Leu Pro Gln Leu Cys Asp Phe Thr Val Ala Asp
 1140 1145 1150
 Thr Arg Arg Tyr Arg Thr Ser Gly Ser Asp Glu Glu Gln Glu Gly Ala
 1155 1160 1165
 Gly Ala Ile Asn Gln Asn Val Ala Leu Ala Ile Ala Gly Asn Asn Phe
 1170 1175 1180
 Asn Leu Lys Thr Ser Gly Ile Val Leu Ser Ser Leu Pro Tyr Lys Gln
 1185 1190 1195 1200
 Tyr Asn Met Leu Asn Ala Asp Thr Thr Arg Asn Leu Met Ile Cys Phe
 1205 1210 1215
 Leu Trp Ile Met Lys Asn Ala Asp Gln Ser Leu Ile Arg Lys Trp Ile
 1220 1225 1230
 Ala Asp Leu Pro Ser Thr Gln Leu Asn Arg Ile Leu Asp Leu Leu Phe
 1235 1240 1245
 Ile Cys Val Leu Cys Phe Glu Tyr Lys Gly Lys Gln Ser Ser Asp Lys
 1250 1255 1260
 Val Ser Thr Gln Val Leu Gln Lys Ser Arg Asp Val Lys Ala Arg Leu
 1265 1270 1275 1280
 Glu Glu Ala Leu Leu Arg Gly Glu Gly Ala Arg Gly Glu Met Met Arg
 1285 1290 1295
 Arg Arg Ala Pro Gly Asn Asp Arg Phe Pro Gly Leu Asn Glu Asn Leu
 1300 1305 1310
 Arg Trp Lys Lys Glu Gln Thr His Trp Arg Gln Ala Asn Glu Lys Leu
 1315 1320 1325
 Asp Lys Thr Lys Ala Glu Leu Asp Gln Glu Ala Leu Ile Ser Gly Asn
 1330 1335 1340

Leu Ala Thr Glu Ala His Leu Ile Ile Leu Asp Met Gln Glu Asn Ile
 1345 1350 1355 1360
 Ile Gln Ala Ser Ser Ala Leu Asp Cys Lys Asp Ser Leu Leu Gly Gly
 1365 1370 1375
 Val Leu Arg Val Leu Val Asn Ser Leu Asn Cys Asp Gln Ser Thr Thr
 1380 1385 1390
 Tyr Leu Thr His Cys Phe Ala Thr Leu Arg Ala Leu Ile Ala Lys Phe
 1395 1400 1405
 Gly Asp Leu Leu Phe Glu Glu Glu Val Glu Gln Cys Phe Asp Leu Cys
 1410 1415 1420
 His Gln Val Leu His His Cys Ser Ser Ser Met Asp Val Thr Arg Ser
 1425 1430 1435 1440
 Gln Ala Cys Ala Thr Leu Tyr Leu Leu Met Arg Phe Ser Phe Gly Ala
 1445 1450 1455
 Thr Ser Asn Phe Ala Arg Val Lys Met Gln Val Thr Met Ser Leu Ala
 1460 1465 1470
 Ser Leu Val Gly Arg Ala Pro Asp Phe Asn Glu Glu His Leu Arg Arg
 1475 1480 1485
 Ser Leu Arg Thr Ile Leu Ala Tyr Ser Glu Glu Asp Thr Ala Met Gln
 1490 1495 1500
 Met Thr Pro Phe Pro Thr Gln Val Glu Glu Leu Leu Cys Asn Leu Asn
 1505 1510 1515 1520
 Ser Ile Leu Tyr Asp Thr Val Lys Met Arg Glu Phe Gln Glu Asp Pro
 1525 1530 1535
 Glu Met Leu Met Asp Leu Met Tyr Arg Ile Ala Lys Ser Tyr Gln Ala
 1540 1545 1550
 Ser Pro Asp Leu Arg Leu Thr Trp Leu Gln Asn Met Ala Glu Lys His
 1555 1560 1565
 Thr Lys Lys Lys Cys Tyr Thr Glu Ala Ala Met Cys Leu Val His Ala
 1570 1575 1580
 Ala Ala Leu Val Ala Glu Tyr Leu Ser Met Leu Glu Asp His Ser Tyr
 1585 1590 1595 1600
 Leu Pro Val Gly Ser Val Ser Phe Gln Asn Ile Ser Ser Asn Val Leu
 1605 1610 1615
 Glu Glu Ser Val Val Ser Glu Asp Thr Leu Ser Pro Asp Glu Asp Gly
 1620 1625 1630
 Val Cys Ala Gly Gln Tyr Phe Thr Glu Ser Gly Leu Val Gly Leu Leu
 1635 1640 1645
 Glu Gln Ala Ala Glu Leu Phe Ser Thr Gly Gly Leu Tyr Glu Thr Val
 1650 1655 1660

Asn Glu Val Tyr Lys Leu Val Ile Pro Ile Leu Glu Ala His Arg Glu
 1665 1670 1675 1680
 Phe Arg Lys Leu Thr Leu Thr His Ser Lys Leu Gln Arg Ala Phe Asp
 1685 1690 1695
 Ser Ile Val Asn Lys Asp His Lys Arg Met Phe Gly Thr Tyr Phe Arg
 1700 1705 1710
 Val Gly Phe Phe Gly Ser Lys Phe Gly Asp Leu Asp Glu Gln Glu Phe
 1715 1720 1725
 Val Tyr Lys Glu Pro Ala Ile Thr Lys Leu Pro Glu Ile Ser His Arg
 1730 1735 1740
 Leu Glu Ala Phe Tyr Gly Gln Cys Phe Gly Ala Glu Phe Val Glu Val
 1745 1750 1755 1760
 Ile Lys Asp Ser Thr Pro Val Asp Lys Thr Lys Leu Asp Pro Asn Lys
 1765 1770 1775
 Ala Tyr Ile Gln Ile Thr Phe Val Glu Pro Tyr Phe Asp Glu Tyr Glu
 1780 1785 1790
 Met Lys Asp Arg Val Thr Tyr Phe Glu Lys Asn Phe Asn Leu Arg Arg
 1795 1800 1805
 Phe Met Tyr Thr Thr Pro Phe Thr Leu Glu Gly Arg Pro Arg Gly Glu
 1810 1815 1820
 Leu His Glu Gln Tyr Arg Arg Asn Thr Val Leu Thr Thr Met His Ala
 1825 1830 1835 1840
 Phe Pro Tyr Ile Lys Thr Arg Ile Ser Val Ile Gln Lys Glu Glu Phe
 1845 1850 1855
 Val Leu Thr Pro Ile Glu Val Ala Ile Glu Asp Met Lys Lys Lys Thr
 1860 1865 1870
 Leu Gln Leu Ala Val Ala Ile Asn Gln Glu Pro Pro Asp Ala Lys Met
 1875 1880 1885
 Leu Gln Met Val Leu Gln Gly Ser Val Gly Ala Thr Val Asn Gln Gly
 1890 1895 1900
 Pro Leu Glu Val Ala Gln Val Phe Leu Ala Glu Ile Pro Ala Asp Pro
 1905 1910 1915 1920
 Lys Leu Tyr Arg His His Asn Lys Leu Arg Leu Cys Phe Lys Glu Phe
 1925 1930 1935
 Ile Met Arg Cys Gly Glu Ala Val Glu Lys Asn Lys Arg Leu Ile Thr
 1940 1945 1950
 Ala Asp Gln Arg Glu Tyr Gln Gln Glu Leu Lys Lys Asn Tyr Asn Lys
 1955 1960 1965
 Leu Lys Glu Asn Leu Arg Pro Met Ile Glu Arg Lys Ile Pro Glu Leu
 1970 1975 1980

Tyr Lys Pro Ile Phe Arg Val Glu Ser Gln Lys Arg Asp Ser Phe His
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Arg Ser Ser Phe Arg Lys Cys Glu Thr Gln Leu Ser Gln Gly Ser
 2005 2010 2015

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<211> 2090

<212> PRT

<213> Homo sapiens

<220>

<223> human CLASP-3

<400> 107

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Leu Leu Lys Asn Leu Asn Ile Val Gly Asn Ile Ser His His Thr Thr
 35 40 45

Val Pro Leu Thr Glu Ala Val Asp Pro Val Asp Leu Glu Asp Tyr Leu
 50 55 60

Ile Thr His Pro Leu Ala Val Asp Ser Gly Pro Leu Arg Asp Leu Ile
 65 70 75 80

Glu Phe Pro Pro Asp Asp Ile Glu Val Val Tyr Ser Pro Arg Asp Cys
 85 90 95

Arg Thr Leu Val Ser Ala Val Pro Glu Glu Ser Glu Met Asp Pro His
 100 105 110

Val Arg Asp Cys Ile Arg Ser Tyr Thr Glu Asp Trp Ala Ile Val Ile
 115 120 125

Arg Lys Tyr His Lys Leu Gly Thr Gly Phe Asn Pro Asn Thr Leu Asp
 130 135 140

Lys Gln Lys Glu Arg Gln Lys Gly Leu Pro Lys Gln Val Phe Glu Ser
 145 150 155 160

Asp Glu Ala Pro Asp Gly Asn Ser Tyr Gln Asp Asp Gln Asp Asp Leu
 165 170 175

Lys Arg Arg Ser Met Ser Ile Asp Asp Thr Pro Arg Gly Ser Trp Ala
 180 185 190

Cys Ser Ile Phe Asp Leu Lys Asn Ser Leu Pro Asp Ala Leu Leu Pro
 195 200 205

Asn Leu Leu Asp Arg Thr Pro Asn Glu Glu Ile Asp Arg Gln Asn Asp
 210 215 220

Asp Gln Arg Lys Ser Asn Arg His Lys Glu Leu Phe Ala Leu His Pro
 225 230 235 240

Ser Pro Asp Glu Glu Glu Pro Ile Glu Arg Leu Ser Val Pro Asp Ile
 245 250 255
 Pro Lys Glu His Phe Gly Gln Arg Leu Leu Val Lys Cys Leu Ser Leu
 260 265 270
 Lys Phe Glu Ile Glu Ile Glu Pro Ile Phe Ala Ser Leu Ala Leu Tyr
 275 280 285
 Asp Val Lys Glu Lys Lys Lys Ile Ser Glu Asn Phe Tyr Phe Asp Leu
 290 295 300
 Asn Ser Glu Gln Met Lys Gly Leu Leu Arg Pro His Val Pro Pro Ala
 305 310 315 320
 Ala Ile Thr Thr Leu Ala Arg Ser Ala Ile Phe Ser Ile Thr Tyr Pro
 325 330 335
 Ser Gln Asp Val Phe Leu Val Ile Lys Leu Glu Lys Val Leu Gln Gln
 340 345 350
 Gly Asp Ile Gly Glu Cys Ala Glu Pro Tyr Met Ile Phe Lys Glu Ala
 355 360 365
 Asp Ala Thr Lys Asn Lys Glu Lys Leu Glu Lys Leu Lys Ser Gln Ala
 370 375 380
 Asp Gln Phe Cys Gln Arg Leu Gly Lys Tyr Arg Met Pro Phe Ala Trp
 385 390 395 400
 Thr Ala Ile His Leu Met Asn Ile Val Ser Ser Ala Gly Ser Leu Glu
 405 410 415
 Arg Asp Ser Thr Glu Val Glu Ile Ser Thr Gly Glu Arg Lys Gly Ser
 420 425 430
 Trp Ser Glu Arg Arg Asn Ser Ser Ile Val Gly Arg Arg Ser Leu Glu
 435 440 445
 Arg Thr Thr Ser Gly Asp Asp Ala Cys Asn Leu Thr Ser Phe Arg Pro
 450 455 460
 Ala Thr Leu Thr Val Thr Asn Phe Phe Lys Gln Glu Gly Asp Arg Leu
 465 470 475 480
 Ser Asp Glu Asp Leu Tyr Lys Phe Leu Ala Asp Met Arg Arg Pro Ser
 485 490 495
 Ser Val Leu Arg Arg Leu Arg Pro Ile Thr Ala Gln Leu Lys Ile Asp
 500 505 510
 Ile Ser Pro Ala Pro Glu Asn Pro His Tyr Cys Leu Thr Pro Glu Leu
 515 520 525
 Leu Gln Val Lys Leu Tyr Pro Asp Ser Arg Val Arg Pro Thr Arg Glu
 530 535 540
 Ile Leu Glu Phe Pro Ala Arg Asp Val Tyr Val Pro Asn Thr Thr Tyr
 545 550 555 560

Arg Asn Leu Leu Tyr Ile Tyr Pro Gln Ser Leu Asn Phe Ala Asn Arg
 565 570 575
 Gln Gly Ser Ala Arg Asn Ile Thr Val Lys Val Gln Phe Met Tyr Gly
 580 585 590
 Glu Asp Pro Ser Asn Ala Met Pro Val Ile Phe Gly Lys Ser Ser Cys
 595 600 605
 Ser Glu Phe Ser Lys Glu Ala Tyr Thr Ala Val Val Tyr His Asn Arg
 610 615 620
 Ser Pro Asp Phe His Glu Glu Ile Lys Val Lys Leu Pro Ala Thr Leu
 625 630 635 640
 Thr Asp His His His Leu Leu Phe Thr Phe Tyr His Val Ser Cys Gln
 645 650 655
 Gln Lys Gln Asn Thr Pro Leu Glu Thr Pro Val Gly Tyr Thr Trp Ile
 660 665 670
 Pro Met Leu Gln Asn Gly Arg Leu Lys Thr Gly Gln Phe Cys Leu Pro
 675 680 685
 Val Ser Leu Glu Lys Pro Pro Gln Ala Tyr Ser Val Leu Ser Pro Glu
 690 695 700
 Val Pro Leu Pro Gly Met Lys Trp Val Asp Asn His Lys Gly Val Phe
 705 710 715 720
 Asn Val Glu Val Val Ala Val Ser Ser Ile His Thr Gln Asp Pro Tyr
 725 730 735
 Leu Asp Lys Phe Phe Ala Leu Val Asn Ala Leu Asp Glu His Leu Phe
 740 745 750
 Pro Val Arg Ile Gly Asp Met Arg Ile Met Glu Asn Asn Leu Glu Asn
 755 760 765
 Glu Leu Lys Ser Ser Ile Ser Ala Leu Asn Ser Ser Gln Leu Glu Pro
 770 775 780
 Val Val Arg Phe Leu His Leu Leu Leu Asp Lys Leu Ile Leu Leu Val
 785 790 795 800
 Ile Arg Pro Pro Val Ile Ala Gly Gln Ile Val Asn Leu Gly Gln Ala
 805 810 815
 Ser Phe Glu Ala Met Ala Ser Ile Ile Asn Arg Leu His Lys Asn Leu
 820 825 830
 Glu Gly Asn His Asp Gln His Gly Arg Asn Ser Leu Leu Ala Ser Tyr
 835 840 845
 Ile His Tyr Val Phe Arg Leu Pro Asn Thr Tyr Pro Asn Ser Ser Ser
 850 855 860
 Pro Gly Pro Gly Gly Leu Gly Gly Ser Val His Tyr Ala Thr Met Ala
 865 870 875 880

Arg Ser Ala Val Arg Pro Ala Ser Leu Asn Leu Asn Arg Ser Arg Ser
 885 890 895
 Leu Ser Asn Ser Asn Pro Asp Ile Ser Gly Thr Pro Thr Ser Pro Asp
 900 905 910
 Asp Glu Val Arg Ser Ile Ile Gly Ser Lys Gly Leu Asp Arg Ser Asn
 915 920 925
 Ser Trp Val Asn Thr Gly Gly Pro Lys Ala Ala Pro Trp Gly Ser Asn
 930 935 940
 Pro Ser Pro Ser Ala Glu Ser Thr Gln Ala Met Asp Arg Ser Cys Asn
 945 950 955 960
 Arg Met Ser Ser His Thr Glu Thr Ser Ser Phe Leu Gln Thr Leu Thr
 965 970 975
 Gly Arg Leu Pro Thr Lys Lys Leu Phe His Glu Glu Leu Ala Leu Gln
 980 985 990
 Trp Val Val Cys Ser Gly Ser Val Arg Glu Ser Ala Leu Gln Gln Ala
 995 1000 1005
 Trp Phe Phe Phe Glu Leu Met Val Lys Ser Met Val His His Leu Tyr
 1010 1015 1020
 Phe Asn Asp Lys Leu Glu Ala Pro Arg Lys Ser Arg Phe Pro Glu Arg
 1025 1030 1035 1040
 Phe Met Asp Asp Ile Ala Ala Leu Val Ser Thr Ile Ala Ser Asp Ile
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 Val Ser Arg Phe Gln Lys Asp Thr Glu Met Val Glu Arg Leu Asn Thr
 1060 1065 1070
 Ser Leu Ala Phe Phe Leu Asn Asp Leu Leu Ser Val Met Asp Arg Gly
 1075 1080 1085
 Phe Val Phe Ser Leu Ile Lys Ser Cys Tyr Lys Gln Val Ser Ser Lys
 1090 1095 1100
 Leu Tyr Ser Leu Pro Asn Pro Ser Val Leu Val Ser Leu Arg Leu Asp
 1105 1110 1115 1120
 Phe Leu Arg Ile Ile Cys Ser His Glu His Tyr Val Thr Leu Asn Leu
 1125 1130 1135
 Pro Cys Ser Leu Leu Thr Pro Pro Ala Ser Pro Ser Pro Ser Val Ser
 1140 1145 1150
 Ser Ala Thr Ser Gln Ser Ser Gly Phe Ser Thr Asn Val Gln Asp Gln
 1155 1160 1165
 Lys Ile Ala Asn Met Phe Glu Leu Ser Val Pro Phe Arg Gln Gln His
 1170 1175 1180
 Tyr Leu Ala Gly Leu Val Leu Thr Glu Leu Ala Val Ile Leu Asp Pro
 1185 1190 1195 1200

Asp Ala Glu Gly Leu Phe Gly Leu His Lys Lys Val Ile Asn Met Val
 1205 1210 1215
 His Asn Leu Leu Ser Ser His Asp Ser Asp Pro Arg Tyr Ser Asp Pro
 1220 1225 1230
 Gln Ile Lys Ala Arg Val Ala Met Leu Tyr Leu Pro Leu Ile Gly Ile
 1235 1240 1245
 Ile Met Glu Thr Val Pro Gln Leu Tyr Asp Phe Thr Glu Thr His Asn
 1250 1255 1260
 Gln Arg Gly Arg Pro Ile Cys Ile Ala Thr Asp Asp Tyr Glu Ser Glu
 1265 1270 1275 1280
 Ser Gly Ser Met Ile Ser Gln Thr Val Ala Met Ala Ile Ala Gly Thr
 1285 1290 1295
 Ser Val Pro Gln Leu Thr Arg Pro Gly Ser Phe Leu Leu Thr Ser Thr
 1300 1305 1310
 Ser Gly Arg Gln His Thr Thr Phe Ser Ala Glu Ser Ser Arg Ser Leu
 1315 1320 1325
 Leu Ile Cys Leu Leu Trp Val Leu Lys Asn Ala Asp Glu Thr Val Leu
 1330 1335 1340
 Gln Lys Trp Phe Thr Asp Leu Ser Val Leu Gln Leu Asn Arg Leu Leu
 1345 1350 1355 1360
 Asp Leu Leu Tyr Leu Cys Val Ser Cys Phe Glu Tyr Lys Gly Lys Lys
 1365 1370 1375
 Val Phe Glu Arg Met Asn Ser Leu Thr Phe Lys Lys Ser Lys Asp Met
 1380 1385 1390
 Arg Ala Lys Leu Glu Glu Ala Ile Leu Gly Ser Ile Gly Ala Arg Gln
 1395 1400 1405
 Glu Met Val Arg Arg Ser Arg Gly Gln Leu Glu Arg Ser Pro Ser Gly
 1410 1415 1420
 Ser Ala Phe Gly Ser Gln Glu Asn Leu Arg Trp Arg Lys Asp Met Thr
 1425 1430 1435 1440
 His Trp Arg Gln Asn Thr Glu Lys Leu Asp Lys Ser Arg Ala Glu Ile
 1445 1450 1455
 Glu His Glu Ala Leu Ile Asp Gly Asn Leu Ala Thr Glu Ala Asn Leu
 1460 1465 1470
 Ile Ile Leu Asp Thr Leu Glu Ile Val Val Gln Thr Val Ser Val Thr
 1475 1480 1485
 Glu Ser Lys Glu Ser Ile Leu Gly Gly Val Leu Lys Val Leu Leu His
 1490 1495 1500
 Ser Met Ala Cys Asn Gln Ser Ala Val Tyr Leu Gln His Cys Phe Ala
 1505 1510 1515 1520

Thr Gln Arg Ala Leu Val Ser Lys Phe Pro Glu Leu Leu Phe Glu Glu
 1525 1530 1535
 Glu Thr Glu Gln Cys Ala Asp Leu Cys Leu Arg Leu Leu Arg His Cys
 1540 1545 1550
 Ser Ser Ser Ile Gly Thr Ile Arg Ser His Pro Ser Ala Ser Leu Tyr
 1555 1560 1565
 Leu Leu Met Arg Gln Asn Phe Glu Ile Gly Asn Asn Phe Ala Arg Val
 1570 1575 1580
 Lys Met Gln Val Pro Met Ser Leu Ser Ser Leu Val Gly Thr Ser Gln
 1585 1590 1595 1600
 Asn Phe Asn Glu Glu Phe Leu Arg Arg Ser Leu Lys Thr Ile Leu Thr
 1605 1610 1615
 Tyr Ala Glu Glu Asp Leu Glu Leu Arg Glu Thr Thr Phe Pro Asp Gln
 1620 1625 1630
 Val Gln Asp Leu Val Phe Asn Leu His Met Ile Leu Ser Asp Thr Val
 1635 1640 1645
 Lys Met Lys Glu His Gln Glu Asp Pro Glu Met Leu Ile Asp Leu Met
 1650 1655 1660
 Tyr Arg Ile Ala Lys Gly Tyr Gln Thr Ser Pro Glu Arg Leu Thr Trp
 1665 1670 1675 1680
 Leu Gln Asn Met Ala Gly Lys His Ser Glu Arg Ser Asn His Ala Glu
 1685 1690 1695
 Ala Ala Gln Cys Leu Val His Ser Ala Ala Leu Val Ala Glu Tyr Leu
 1700 1705 1710
 Ser Met Leu Glu Asp Arg Lys Tyr Leu Pro Val Gly Cys Val Thr Phe
 1715 1720 1725
 Gln Asn Ile Ser Ser Asn Val Leu Glu Glu Ser Ala Val Ser Asp Asp
 1730 1735 1740
 Val Val Ser Pro Asp Glu Glu Gly Ile Cys Ser Gly Lys Tyr Phe Thr
 1745 1750 1755 1760
 Glu Ser Gly Leu Val Gly Leu Leu Glu Gln Ala Ala Ala Ser Phe Ser
 1765 1770 1775
 Met Ala Gly Met Tyr Glu Ala Val Asn Glu Val Tyr Lys Val Leu Ile
 1780 1785 1790
 Pro Ile His Glu Ala Asn Arg Asp Ala Lys Lys Leu Ser Thr Ile His
 1795 1800 1805
 Gly Lys Leu Gln Glu Ala Phe Ser Lys Ile Val His Gln Ser Thr Gly
 1810 1815 1820
 Trp Glu Arg Met Phe Gly Thr Tyr Phe Arg Val Gly Phe Tyr Gly Thr
 1825 1830 1835 1840

Lys Phe Gly Asp Leu Asp Glu Gln Glu Phe Val Tyr Lys Glu Pro Ala
 1845 1850 1855
 Ile Thr Lys Leu Ala Glu Ile Ser His Arg Leu Glu Gly Phe Tyr Gly
 1860 1865 1870
 Glu Arg Phe Gly Glu Asp Val Val Glu Val Ile Lys Asp Ser Asn Pro
 1875 1880 1885
 Val Asp Lys Cys Lys Leu Asp Pro Asn Lys Ala Tyr Ile Gln Ile Thr
 1890 1895 1900
 Tyr Val Glu Pro Tyr Phe Asp Thr Tyr Glu Met Lys Asp Arg Ile Thr
 1905 1910 1915 1920
 Tyr Phe Asp Lys Asn Tyr Asn Leu Arg Arg Phe Met Tyr Cys Thr Pro
 1925 1930 1935
 Phe Thr Leu Asp Gly Arg Ala His Gly Glu Leu His Glu Gln Phe Lys
 1940 1945 1950
 Arg Lys Thr Ile Leu Thr Thr Ser His Ala Phe Pro Tyr Ile Lys Thr
 1955 1960 1965
 Arg Val Asn Val Thr His Lys Glu Glu Ile Ile Leu Thr Pro Ile Glu
 1970 1975 1980
 Val Ala Ile Glu Asp Met Gln Lys Lys Thr Gln Glu Leu Ala Phe Ala
 1985 1990 1995 2000
 Thr His Gln Asp Pro Ala Asp Pro Lys Met Leu Gln Met Val Leu Gln
 2005 2010 2015
 Gly Ser Val Gly Thr Thr Val Asn Gln Gly Pro Leu Glu Val Ala Gln
 2020 2025 2030
 Val Phe Leu Ser Glu Ile Pro Ser Asp Pro Lys Leu Phe Arg His His
 2035 2040 2045
 Asn Lys Leu Arg Leu Cys Phe Lys Asp Phe Thr Lys Arg Cys Glu Asp
 2050 2055 2060
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 Gln Arg Glu Leu Gly Lys Leu Ser Ser Pro
 2085 2090

<210> 108

<211> 1980

<212> PRT

<213> Homo sapiens

<220>

<223> human CLASP-2

<400> 108

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 Ala Gln Ser Leu Phe Val Thr Glu Cys Ile Lys Thr Tyr Asn Ser Asp
 35 40 45
 Trp His Leu Val Asn Tyr Lys Tyr Glu Asp Tyr Ser Gly Glu Phe Arg
 50 55 60
 Gln Leu Pro Asn Lys Val Val Lys Leu Asp Lys Leu Pro Val His Val
 65 70 75 80
 Tyr Glu Val Asp Glu Glu Val Asp Lys Asp Glu Asp Ala Ala Ser Leu
 85 90 95
 Gly Ser Gln Lys Gly Gly Ile Thr Lys His Gly Trp Leu Tyr Lys Gly
 100 105 110
 Asn Met Asn Ser Ala Ile Ser Val Thr Met Arg Ser Phe Lys Arg Arg
 115 120 125
 Phe Phe His Leu Ile Gln Leu Gly Asp Gly Ser Tyr Asn Leu Asn Phe
 130 135 140
 Tyr Lys Asp Glu Lys Ile Ser Lys Glu Pro Lys Gly Ser Ile Phe Leu
 145 150 155 160
 Asp Ser Cys Met Gly Val Val Gln Asn Asn Lys Val Arg Arg Phe Ala
 165 170 175
 Phe Glu Leu Lys Met Gln Asp Lys Ser Ser Tyr Leu Leu Ala Ala Asp
 180 185 190
 Ser Glu Val Glu Met Glu Glu Trp Ile Thr Ile Leu Asn Lys Ile Leu
 195 200 205
 Gln Leu Asn Phe Glu Ala Ala Met Gln Glu Lys Arg Asn Gly Asp Ser
 210 215 220
 His Glu Asp Asp Glu Gln Ser Lys Leu Glu Gly Ser Gly Ser Gly Leu
 225 230 235 240
 Asp Ser Tyr Leu Pro Glu Leu Ala Lys Ser Ala Arg Glu Ala Glu Ile
 245 250 255
 Lys Leu Lys Ser Glu Ser Arg Val Lys Leu Phe Tyr Leu Asp Pro Asp
 260 265 270
 Ala Gln Lys Leu Asp Phe Ser Ser Ala Glu Pro Glu Val Lys Ser Phe
 275 280 285
 Glu Glu Lys Phe Gly Lys Arg Ile Leu Val Lys Cys Asn Asp Leu Ser
 290 295 300
 Phe Asn Leu Gln Cys Cys Val Ala Glu Asn Glu Glu Gly Pro Thr Thr
 305 310 315 320
 Asn Val Glu Pro Phe Phe Val Thr Leu Ser Leu Phe Asp Ile Lys Tyr
 325 330 335

Asn Arg Lys Ile Ser Ala Asp Phe His Val Asp Leu Asn His Phe Ser
 340 345 350
 Val Arg Gln Met Leu Ala Thr Thr Ser Pro Ala Leu Met Asn Gly Ser
 355 360 365
 Gly Gln Scr Pro Ser Val Leu Lys Gly Ile Leu His Glu Ala Ala Met
 370 375 380
 Gln Tyr Pro Lys Gln Gly Ile Phe Ser Val Thr Cys Pro His Pro Asp
 385 390 395 400
 Ile Phe Leu Val Ala Arg Ile Glu Lys Val Leu Gln Gly Ser Ile Thr
 405 410 415
 His Cys Ala Glu Pro Tyr Met Lys Ser Ser Asp Ser Ser Lys Val Ala
 420 425 430
 Gln Lys Val Leu Lys Asn Ala Lys Gln Ala Cys Gln Arg Leu Gly Gln
 435 440 445
 Tyr Arg Met Pro Phe Ala Trp Ala Ala Arg Thr Leu Phe Lys Asp Ala
 450 455 460
 Ser Gly Asn Leu Asp Lys Asn Ala Arg Phe Ser Ala Ile Tyr Arg Gln
 465 470 475 480
 Asp Ser Asn Lys Leu Ser Asn Asp Asp Met Leu Lys Leu Leu Ala Asp
 485 490 495
 Phe Arg Lys Pro Glu Lys Met Ala Lys Leu Pro Val Ile Leu Gly Asn
 500 505 510
 Leu Asp Ile Thr Ile Asp Asn Val Ser Ser Asp Phe Pro Asn Tyr Val
 515 520 525
 Asn Ser Ser Tyr Ile Pro Thr Lys Gln Phe Glu Thr Cys Ser Lys Thr
 530 535 540
 Pro Ile Thr Phe Glu Val Glu Glu Phe Val Pro Cys Ile Pro Lys His
 545 550 555 560
 Thr Gln Pro Tyr Thr Ile Tyr Thr Asn His Leu Tyr Val Tyr Pro Lys
 565 570 575
 Tyr Leu Lys Tyr Asp Ser Gln Lys Ser Phe Ala Lys Ala Arg Asn Ile
 580 585 590
 Ala Ile Cys Ile Glu Phe Lys Asp Ser Asp Glu Glu Asp Ser Gln Pro
 595 600 605
 Leu Lys Cys Ile Tyr Gly Arg Pro Gly Gly Pro Val Phe Thr Arg Ser
 610 615 620
 Ala Phe Ala Ala Val Leu His His His Gln Asn Pro Glu Phe Tyr Asp
 625 630 635 640
 Glu Ile Lys Ile Glu Leu Pro Thr Gln Leu His Glu Lys His His Leu
 645 650 655

Leu	Leu	Thr	Phe	Phe	His	Val	Ser	Cys	Asp	Asn	Ser	Ser	Lys	Gly	Ser		
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Thr	Lys	Lys	Arg	Asp	Val	Val	Glu	Thr	Gln	Val	Gly	Tyr	Ser	Trp	Leu		
		675					680					685					
Pro	Leu	Leu	Lys	Asp	Gly	Arg	Val	Val	Thr	Ser	Glu	Gln	His	Ile	Pro		
	690					695					700						
Val	Ser	Ala	Asn	Leu	Pro	Ser	Gly	His	Leu	Gly	Tyr	Gln	Glu	Leu	Gly		
705					710					715					720		
Met	Gly	Arg	His	Tyr	Gly	Pro	Glu	Ile	Lys	Trp	Val	Asp	Gly	Gly	Lys		
				725					730					735			
Pro	Leu	Leu	Lys	Ile	Ser	Thr	His	Leu	Val	Ser	Thr	Val	Tyr	Thr	Gln		
			740					745					750				
Asp	Gln	His	Leu	His	Asn	Phe	Phe	Gln	Tyr	Cys	Gln	Lys	Thr	Glu	Ser		
		755					760					765					
Gly	Ala	Gln	Ala	Leu	Gly	Asn	Glu	Leu	Val	Lys	Tyr	Leu	Lys	Ser	Leu		
	770					775					780						
His	Ala	Met	Glu	Gly	His	Val	Met	Ile	Ala	Phe	Leu	Pro	Thr	Ile	Leu		
785					790					795					800		
Asn	Gln	Leu	Phe	Arg	Val	Leu	Thr	Arg	Ala	Thr	Gln	Glu	Glu	Val	Ala		
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			820					825					830				
Glu	Gly	Leu	Glu	Ser	His	Leu	Arg	Ser	Tyr	Val	Lys	Tyr	Ala	Tyr	Lys		
		835					840					845					
Ala	Glu	Pro	Tyr	Val	Ala	Ser	Glu	Tyr	Lys	Thr	Val	His	Glu	Glu	Leu		
	850					855						860					
Thr	Lys	Ser	Met	Thr	Thr	Ile	Leu	Lys	Pro	Ser	Ala	Asp	Phe	Leu	Thr		
865					870					875					880		
Ser	Asn	Lys	Leu	Leu	Arg	Tyr	Ser	Trp	Phe	Phe	Phe	Asp	Val	Leu	Ile		
				885					890					895			
Lys	Ser	Met	Ala	Gln	His	Leu	Ile	Glu	Asn	Ser	Lys	Val	Lys	Leu	Leu		
			900					905					910				
Arg	Asn	Gln	Arg	Phe	Pro	Ala	Ser	Tyr	His	His	Ala	Ala	Glu	Thr	Val		
		915					920					925					
Val	Asn	Met	Leu	Met	Pro	His	Ile	Thr	Gln	Lys	Phe	Gly	Asp	Asn	Pro		
	930					935					940						
Glu	Ala	Ser	Lys	Asn	Ala	Asn	His	Ser	Leu	Ala	Val	Phe	Ile	Lys	Arg		
945					950					955					960		
Cys	Phe	Thr	Phe	Met	Asp	Arg	Gly	Phe	Val	Phe	Lys	Gln	Ile	Asn	Asn		
				965					970					975			

Tyr Ile Ser Cys Phe Ala Pro Gly Asp Pro Lys Thr Leu Phe Glu Tyr
 980 985 990
 Lys Phe Glu Phe Leu Arg Val Val Cys Asn His Glu His Tyr Ile Pro
 995 1000 1005
 Leu Asn Leu Pro Met Pro Phe Gly Lys Gly Arg Ile Gln Arg Tyr Gln
 1010 1015 1020
 Asp Leu Gln Leu Asp Tyr Ser Leu Thr Asp Glu Phe Cys Arg Asn His
 1025 1030 1035 1040
 Phe Leu Val Gly Leu Leu Arg Glu Val Gly Thr Ala Leu Gln Glu
 1045 1050 1055
 Phe Arg Glu Val Arg Leu Ile Ala Ile Ser Val Leu Lys Asn Leu Leu
 1060 1065 1070
 Ile Lys His Ser Phe Asp Asp Arg Tyr Ala Ser Arg Ser His Gln Ala
 1075 1080 1085
 Arg Ile Ala Thr Leu Tyr Leu Pro Leu Phe Gly Leu Leu Ile Glu Asn
 1090 1095 1100
 Val Gln Arg Ile Asn Val Arg Asp Val Ser Pro Phe Pro Val Asn Ala
 1105 1110 1115 1120
 Gly Met Thr Val Lys Asp Glu Ser Leu Ala Leu Pro Ala Val Asn Pro
 1125 1130 1135
 Leu Val Thr Pro Gln Lys Gly Ser Thr Leu Asp Asn Ser Leu His Lys
 1140 1145 1150
 Asp Leu Leu Gly Ala Ile Ser Gly Ile Ala Ser Pro Tyr Thr Thr Ser
 1155 1160 1165
 Thr Pro Asn Ile Asn Ser Val Arg Asn Ala Asp Ser Arg Gly Ser Leu
 1170 1175 1180
 Ile Ser Thr Asp Ser Gly Asn Ser Leu Pro Glu Arg Asn Ser Glu Lys
 1185 1190 1195 1200
 Ser Asn Ser Leu Asp Lys His Gln Gln Ser Ser Thr Leu Gly Asn Ser
 1205 1210 1215
 Val Val Arg Cys Asp Lys Leu Asp Gln Ser Glu Ile Lys Ser Leu Leu
 1220 1225 1230
 Met Cys Phe Leu Tyr Ile Leu Lys Ser Met Ser Asp Asp Ala Leu Phe
 1235 1240 1245
 Thr Tyr Trp Asn Lys Ala Ser Thr Ser Glu Leu Met Asp Phe Phe Thr
 1250 1255 1260
 Ile Ser Glu Val Cys Leu His Gln Phe Gln Tyr Met Gly Lys Arg Tyr
 1265 1270 1275 1280
 Ile Ala Arg Asn Gln Glu Gly Leu Gly Pro Ile Val His Asp Arg Lys
 1285 1290 1295

Ser Gln Thr Leu Pro Val Ser Arg Asn Arg Thr Gly Met Met His Ala
 1300 1305 1310
 Arg Leu Gln Gln Leu Gly Ser Leu Asp Asn Ser Leu Thr Phe Asn His
 1315 1320 1325
 Ser Tyr Gly His Ser Asp Ala Asp Val Leu His Gln Ser Leu Leu Glu
 1330 1335 1340
 Ala Asn Ile Ala Thr Glu Val Cys Leu Thr Ala Leu Asp Thr Leu Ser
 1345 1350 1355 1360
 Leu Phe Thr Leu Ala Phe Lys Asn Gln Leu Leu Ala Asp His Gly His
 1365 1370 1375
 Asn Pro Leu Met Lys Lys Val Phe Asp Val Tyr Leu Cys Phe Leu Gln
 1380 1385 1390
 Lys His Gln Ser Glu Thr Ala Leu Lys Asn Val Phe Thr Ala Leu Arg
 1395 1400 1405
 Ser Leu Ile Tyr Lys Phe Pro Ser Thr Phe Tyr Glu Gly Arg Ala Asp
 1410 1415 1420
 Met Cys Ala Ala Leu Cys Tyr Glu Ile Leu Lys Cys Cys Asn Ser Lys
 1425 1430 1435 1440
 Leu Ser Ser Ile Arg Thr Glu Ala Ser Gln Leu Leu Tyr Phe Leu Met
 1445 1450 1455
 Arg Asn Asn Phe Asp Tyr Thr Gly Lys Lys Ser Phe Val Arg Thr His
 1460 1465 1470
 Leu Gln Val Ile Ile Ser Val Ser Gln Leu Ile Ala Asp Val Val Gly
 1475 1480 1485
 Ile Gly Glu Thr Arg Phe Gln Gln Ser Leu Ser Ile Ile Asn Asn Cys
 1490 1495 1500
 Ala Asn Ser Asp Arg Leu Ile Lys His Thr Ser Phe Ser Ser Asp Val
 1505 1510 1515 1520
 Lys Asp Leu Thr Lys Arg Ile Arg Thr Val Leu Met Ala Thr Ala Gln
 1525 1530 1535
 Met Lys Glu His Glu Asn Asp Pro Glu Met Leu Val Asp Leu Gln Tyr
 1540 1545 1550
 Ser Leu Ala Lys Ser Tyr Ala Ser Thr Pro Glu Leu Arg Lys Thr Trp
 1555 1560 1565
 Leu Asp Ser Met Ala Arg Ile His Val Lys Asn Gly Asp Leu Ser Glu
 1570 1575 1580
 Ala Ala Met Cys Tyr Val His Val Thr Ala Leu Val Ala Glu Tyr Leu
 1585 1590 1595 1600
 Thr Arg Lys Gly Val Phe Arg Gln Gly Cys Thr Ala Phe Arg Val Ile
 1605 1610 1615

Thr Pro Asn Ile Asp Glu Glu Ala Ser Met Met Glu Asp Val Gly Met
 1620 1625 1630
 Gln Asp Val His Phe Asn Glu Asp Val Leu Met Glu Leu Leu Glu Gln
 1635 1640 1645
 Cys Ala Asp Gly Leu Trp Lys Ala Glu Arg Tyr Glu Leu Ile Ala Asp
 1650 1655 1660
 Ile Tyr Lys Leu Ile Ile Pro Ile Tyr Glu Lys Arg Arg Asp Phe Phe
 1665 1670 1675 1680
 Glu Asp Glu Asp Gly Lys Glu Tyr Ile Tyr Lys Glu Pro Lys Leu Thr
 1685 1690 1695
 Pro Leu Ser Glu Ile Ser Gln Arg Leu Leu Lys Leu Tyr Ser Asp Lys
 1700 1705 1710
 Phe Gly Ser Glu Asn Val Lys Met Ile Gln Asp Ser Gly Lys Val Asn
 1715 1720 1725
 Pro Lys Asp Leu Asp Ser Lys Tyr Ala Tyr Ile Gln Val Thr His Val
 1730 1735 1740
 Ile Pro Phe Phe Asp Glu Lys Glu Leu Gln Glu Arg Lys Thr Glu Phe
 1745 1750 1755 1760
 Glu Arg Ser His Asn Ile Arg Arg Phe Met Phe Glu Met Pro Phe Thr
 1765 1770 1775
 Gln Thr Gly Lys Arg Gln Gly Gly Val Glu Glu Gln Cys Lys Arg Arg
 1780 1785 1790
 Thr Ile Leu Thr Ala Ile His Cys Phe Pro Tyr Val Lys Lys Arg Ile
 1795 1800 1805
 Pro Val Met Tyr Gln His His Thr Asp Leu Asn Pro Ile Glu Val Ala
 1810 1815 1820
 Ile Asp Glu Met Ser Lys Lys Val Ala Glu Leu Arg Gln Leu Cys Ser
 1825 1830 1835 1840
 Ser Ala Glu Val Asp Met Ile Lys Leu Gln Leu Lys Leu Gln Gly Ser
 1845 1850 1855
 Val Ser Val Gln Val Asn Ala Gly Pro Leu Ala Tyr Ala Arg Ala Phe
 1860 1865 1870
 Leu Asp Asp Thr Asn Thr Lys Arg Tyr Pro Asp Asn Lys Val Lys Leu
 1875 1880 1885
 Leu Lys Glu Val Phe Arg Gln Phe Val Glu Ala Cys Gly Gln Ala Leu
 1890 1895 1900
 Ala Val Asn Glu Arg Leu Ile Lys Glu Asp Gln Leu Glu Tyr Gln Glu
 1905 1910 1915 1920
 Glu Met Lys Ala Asn Tyr Arg Glu Met Ala Lys Glu Leu Ser Glu Ile
 1925 1930 1935

Met His Glu Gln Ile Cys Pro Leu Glu Glu Lys Thr Ser Val Leu Pro
1940 1945 1950

Asn Ser Leu His Ile Phe Asn Ala Ile Ser Gly Thr Pro Thr Ser Thr
1955 1960 1965

Met Val His Gly Met Thr Ser Ser Ser Ser Val Val
1970 1975 1980

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<211> 2045

<212> PRT

<213> Homo sapiens

<220>

<223> human CLASP-7

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Pro His Ser Ser Arg Arg Cys Ser Ser Ser Leu Gly Val Pro Leu Thr
35 40 45

Glu Val Val Glu Pro Leu Asp Phe Glu Asp Val Leu Leu Ser Arg Pro
50 55 60

Pro Asp Ala Glu Pro Gly Pro Leu Arg Asp Leu Val Glu Phe Pro Ala
65 70 75 80

Asp Asp Leu Glu Leu Leu Leu Gln Pro Arg Glu Cys Arg Thr Thr Glu
85 90 95

Pro Gly Ile Pro Lys Asp Glu Lys Leu Asp Ala Gln Val Arg Ala Ala
100 105 110

Val Glu Met Tyr Ile Glu Asp Trp Val Ile Val His Arg Arg Tyr Gln
115 120 125

Tyr Leu Ser Ala Ala Tyr Ser Pro Val Thr Thr Asp Thr Gln Arg Glu
130 135 140

Arg Gln Lys Gly Leu Pro Arg Gln Val Phe Glu Gln Asp Ala Ser Gly
145 150 155 160

Asp Glu Arg Ser Gly Pro Glu Asp Ser Asn Asp Ser Arg Arg Gly Ser
165 170 175

Gly Ser Pro Glu Asp Thr Pro Arg Ser Ser Gly Ala Ser Ser Ile Phe
180 185 190

Asp Leu Arg Asn Leu Ala Ala Asp Ser Leu Leu Pro Ser Leu Leu Glu
195 200 205

Arg Ala Ala Pro Glu Asp Val Asp Arg Arg Asn Glu Thr Leu Arg Arg
210 215 220

Gln His Arg Pro Pro Ala Leu Leu Thr Leu Tyr Pro Ala Pro Asp Glu
 225 230 235 240
 Asp Glu Ala Val Glu Arg Cys Ser Arg Pro Glu Pro Pro Arg Glu His
 245 250 255
 Phe Gly Gln Arg Ile Leu Val Lys Cys Leu Ser Leu Lys Phe Glu Ile
 260 265 270
 Glu Ile Glu Pro Ile Phe Gly Ile Leu Ala Leu Tyr Asp Val Arg Glu
 275 280 285
 Lys Lys Lys Ile Ser Glu Asn Phe Tyr Phe Asp Leu Asn Ser Asp Ser
 290 295 300
 Met Lys Gly Leu Leu Arg Ala His Gly Thr His Pro Ala Ile Ser Thr
 305 310 315 320
 Leu Ala Arg Ser Ala Ile Phe Ser Val Thr Tyr Pro Ser Pro Asp Ile
 325 330 335
 Phe Leu Val Ile Lys Leu Glu Lys Val Leu Gln Gln Gly Asp Ile Ser
 340 345 350
 Glu Cys Cys Glu Pro Tyr Met Val Leu Lys Glu Val Asp Thr Ala Lys
 355 360 365
 Asn Lys Glu Lys Leu Glu Lys Leu Arg Leu Ala Ala Glu Gln Phe Cys
 370 375 380
 Thr Arg Leu Gly Arg Tyr Arg Met Pro Phe Ala Trp Thr Ala Val His
 385 390 395 400
 Leu Ala Asn Ile Val Ser Ser Ala Gly Gln Leu Asp Arg Asp Ser Asp
 405 410 415
 Ser Glu Gly Glu Arg Arg Pro Ala Trp Thr Asp Arg Arg Arg Arg Gly
 420 425 430
 Pro Gln Asp Arg Ala Ser Ser Gly Asp Asp Ala Cys Ser Phe Ser Gly
 435 440 445
 Phe Arg Pro Ala Thr Leu Thr Val Thr Asn Phe Phe Lys Gln Glu Ala
 450 455 460
 Glu Arg Leu Ser Asp Glu Asp Leu Phe Lys Phe Leu Ala Asp Met Arg
 465 470 475 480
 Arg Pro Ser Ser Leu Leu Arg Arg Leu Arg Pro Val Thr Ala Gln Leu
 485 490 495
 Lys Ile Asp Ile Ser Pro Ala Pro Glu Asn Pro His Phe Cys Leu Ser
 500 505 510
 Pro Glu Leu Leu His Ile Lys Pro Tyr Pro Asp Pro Arg Gly Arg Pro
 515 520 525
 Thr Lys Glu Ile Leu Glu Phe Pro Ala Arg Glu Val Tyr Ala Pro His
 530 535 540

Thr Ser Tyr Arg Asn Leu Leu Tyr Val Tyr Pro His Ser Leu Asn Phe
 545 550 555 560
 Ser Ser Arg Gln Gly Ser Val Arg Asn Leu Ala Val Arg Val Gln Tyr
 565 570 575
 Met Thr Gly Glu Asp Pro Ser Gln Ala Leu Pro Val Ile Phe Gly Lys
 580 585 590
 Ser Ser Cys Ser Glu Phe Thr Arg Glu Ala Phe Thr Pro Val Val Tyr
 595 600 605
 His Asn Lys Ser Pro Glu Phe Tyr Glu Glu Phe Lys Leu His Leu Pro
 610 615 620
 Ala Cys Val Thr Glu Asn His His Leu Leu Phe Thr Phe Tyr His Val
 625 630 635 640
 Ser Cys Gln Pro Arg Pro Gly Thr Ala Leu Glu Thr Pro Val Gly Phe
 645 650 655
 Thr Trp Ile Pro Leu Leu Gln His Gly Arg Leu Arg Thr Gly Pro Phe
 660 665 670
 Cys Leu Pro Val Ser Val Asp Gln Pro Pro Pro Ser Tyr Ser Val Leu
 675 680 685
 Thr Pro Asp Val Ala Leu Pro Gly Met Arg Trp Val Asp Gly His Lys
 690 695 700
 Gly Val Phe Ser Val Glu Leu Thr Ala Val Ser Ser Val His Pro Gln
 705 710 715 720
 Asp Pro Tyr Leu Asp Lys Phe Phe Thr Leu Val His Val Leu Glu Glu
 725 730 735
 Gly Ala Phe Pro Phe Arg Leu Lys Asp Thr Val Leu Ser Glu Gly Asn
 740 745 750
 Val Glu Gln Glu Leu Arg Ala Ser Leu Ala Ala Leu Arg Leu Ala Ser
 755 760 765
 Pro Glu Pro Leu Val Ala Phe Ser His His Val Leu Asp Lys Leu Val
 770 775 780
 Arg Leu Val Ile Arg Pro Pro Ile Ile Ser Gly Gln Ile Val Asn Leu
 785 790 795 800
 Gly Arg Gly Ala Phe Glu Ala Met Ala His Val Val Ser Leu Val His
 805 810 815
 Arg Ser Leu Glu Ala Ala Gln Asp Ala Arg Gly His Cys Pro Gln Leu
 820 825 830
 Ala Ala Tyr Val His Tyr Ala Phe Arg Leu Pro Gly Thr Glu Pro Ser
 835 840 845
 Leu Pro Asp Gly Ala Pro Pro Val Thr Val Gln Ala Ala Thr Leu Ala
 850 855 860

Arg Gly Ser Gly Arg Pro Ala Ser Leu Tyr Leu Ala Arg Ser Lys Ser
 865 870 875 880
 Ile Ser Ser Ser Asn Pro Asp Leu Ala Val Ala Pro Gly Ser Val Asp
 885 890 895
 Asp Glu Val Ser Arg Ile Leu Ala Ser Lys Leu Leu His Glu Glu Leu
 900 905 910
 Ala Leu Gln Trp Val Val Ser Ser Ser Ala Val Arg Glu Ala Ile Leu
 915 920 925
 Gln His Ala Trp Phe Phe Phe Gln Leu Met Val Lys Ser Met Ala Leu
 930 935 940
 His Leu Leu Leu Gly Gln Arg Leu Asp Thr Pro Arg Lys Leu Arg Phe
 945 950 955 960
 Pro Gly Arg Phe Leu Asp Asp Ile Thr Ala Leu Val Gly Ser Val Gly
 965 970 975
 Leu Glu Val Ile Thr Arg Val His Lys Asp Val Glu Leu Ala Glu His
 980 985 990
 Leu Asn Ala Ser Leu Ala Phe Phe Leu Ser Asp Leu Leu Ser Leu Val
 995 1000 1005
 Asp Arg Gly Phe Val Phe Ser Leu Val Arg Ala His Tyr Lys Gln Val
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 Ala Thr Arg Leu Gln Ser Ser Pro Asn Pro Ala Ala Leu Leu Thr Leu
 1025 1030 1035 1040
 Arg Met Glu Phe Thr Arg Ile Leu Cys Ser His Glu His Tyr Val Thr
 1045 1050 1055
 Leu Asn Leu Pro Cys Cys Pro Leu Ser Pro Pro Ala Ser Pro Ser Pro
 1060 1065 1070
 Ser Val Ser Ser Thr Thr Ser Gln Ser Ser Thr Phe Ser Ser Gln Ala
 1075 1080 1085
 Pro Asp Pro Lys Val Thr Ser Met Phe Glu Leu Ser Gly Pro Phe Arg
 1090 1095 1100
 Gln Gln His Phe Leu Ala Gly Leu Leu Leu Thr Glu Leu Ala Leu Ala
 1105 1110 1115 1120
 Leu Gln Glu Asp Gln Asp Val Arg His Leu Ala Leu Ala Val Leu Lys
 1125 1130 1135
 Asn Leu Met Ala Lys His Ser Phe Asp Asp Arg Tyr Arg Glu Pro Arg
 1140 1145 1150
 Lys Gln Ala Gln Ile Ala Ser Leu Tyr Met Pro Leu Tyr Gly Met Leu
 1155 1160 1165
 Leu Asp Asn Met Pro Arg Ile Arg Leu His Asp Phe Ala Glu Gly Pro
 1170 1175 1180

Gly Gln Arg Ser Arg Leu Ala Ser Met Leu Asp Ser Asp Thr Glu Gly
 1185 1190 1195 1200
 Glu Gly Asp Ile Ala Gly Thr Ile Asn Pro Ser Val Ala Met Ala Ile
 1205 1210 1215
 Ala Gly Gly Pro Leu Ala Pro Gly Ser Arg Ala Ser Ile Ser Gln Gly
 1220 1225 1230
 Pro Pro Thr Ala Ser Arg Ala Gly Cys Ala Leu Ser Ala Glu Ser Ser
 1235 1240 1245
 Arg Thr Leu Leu Ala Cys Val Leu Trp Val Leu Lys Asn Thr Glu Pro
 1250 1255 1260
 Ala Leu Leu Gln Arg Trp Ala Thr Asp Leu Thr Leu Pro Gln Leu Gly
 1265 1270 1275 1280
 Arg Leu Leu Asp Leu Leu Tyr Leu Cys Leu Ala Ala Phe Glu Tyr Lys
 1285 1290 1295
 Gly Lys Lys Ala Phe Glu Arg Ile Asn Ser Leu Thr Phe Lys Lys Ser
 1300 1305 1310
 Leu Asp Met Lys Ala Arg Leu Glu Glu Ala Ile Leu Gly Thr Ile Gly
 1315 1320 1325
 Ala Arg Gln Glu Met Val Arg Arg Ser Arg Glu Arg Ser Pro Phe Gly
 1330 1335 1340
 Asn Pro Glu Asn Val Arg Trp Arg Lys Ser Val Thr His Trp Lys Gln
 1345 1350 1355 1360
 Thr Ser Asp Arg Val Asp Lys Thr Lys Asp Glu Met Glu His Glu Ala
 1365 1370 1375
 Leu Val Glu Gly Asn Leu Ala Thr Glu Ala Ser Leu Val Val Leu Asp
 1380 1385 1390
 Thr Leu Glu Ile Ile Val Gln Thr Val Met Leu Ser Glu Ala Arg Glu
 1395 1400 1405
 Ser Val Leu Gly Ala Val Leu Lys Val Val Leu Tyr Ser Leu Gly Ser
 1410 1415 1420
 Ala Gln Ser Ala Leu Phe Leu Gln His Gly Leu Ala Thr Gln Arg Ala
 1425 1430 1435 1440
 Leu Val Ser Lys Phe Pro Glu Leu Leu Phe Glu Glu Asp Thr Glu Leu
 1445 1450 1455
 Cys Ala Asp Leu Cys Leu Arg Leu Leu Arg His Cys Gly Ser Arg Ile
 1460 1465 1470
 Ser Thr Ile Arg Thr His Ala Ser Ala Ser Leu Tyr Leu Leu Met Arg
 1475 1480 1485
 Gln Asn Phe Glu Ile Gly His Asn Phe Ala Arg Val Lys Met Gln Val
 1490 1495 1500

Thr Met Ser Leu Ser Ser Leu Val Gly Thr Thr Gln Asn Phe Ser Glu
 1505 1510 1515 1520
 Glu His Leu Arg Arg Ser Leu Lys Thr Ile Leu Thr Tyr Ala Glu Glu
 1525 1530 1535
 Asp Met Gly Leu Arg Asp Ser Thr Phe Ala Glu Gln Val Gln Asp Leu
 1540 1545 1550
 Met Phe Asn Leu His Met Ile Leu Thr Asp Thr Val Lys Met Lys Glu
 1555 1560 1565
 His Gln Glu Asp Pro Glu Met Leu Ile Asp Leu Met Tyr Arg Ile Ala
 1570 1575 1580
 Arg Gly Tyr Gln Gly Ser Pro Asp Leu Arg Leu Thr Trp Leu Gln Asn
 1585 1590 1595 1600
 Met Ala Gly Lys His Ala Glu Leu Gly Asn His Ala Glu Ala Ala Gln
 1605 1610 1615
 Cys Met Val His Ala Ala Ala Leu Val Ala Glu Tyr Leu Ala Leu Leu
 1620 1625 1630
 Glu Asp Gln Arg His Leu Pro Val Gly Cys Val Ser Phe Gln Asn Ile
 1635 1640 1645
 Ser Ser Asn Val Leu Glu Glu Ser Ala Ile Ser Asp Asp Ile Leu Ser
 1650 1655 1660
 Pro Asp Glu Glu Gly Phe Cys Ser Gly Lys His Phe Thr Glu Leu Gly
 1665 1670 1675 1680
 Leu Val Gly Leu Leu Glu Gln Ala Ala Gly Tyr Phe Thr Met Gly Gly
 1685 1690 1695
 Leu Tyr Glu Ala Val Asn Glu Val Tyr Lys Asn Leu Ile Pro Ile Leu
 1700 1705 1710
 Glu Ala His Arg Asp Tyr Lys Lys Leu Ala Ala Val His Gly Lys Leu
 1715 1720 1725
 Gln Glu Ala Phe Thr Lys Ile Met His Gln Ser Ser Gly Trp Glu Arg
 1730 1735 1740
 Val Phe Gly Thr Tyr Phe Arg Val Gly Phe Tyr Gly Ala His Phe Gly
 1745 1750 1755 1760
 Asp Leu Asp Glu Gln Glu Phe Val Tyr Lys Glu Pro Ser Ile Thr Lys
 1765 1770 1775
 Leu Ala Glu Ile Ser His Arg Leu Glu Glu Phe Tyr Thr Glu Arg Phe
 1780 1785 1790
 Gly Asp Asp Val Val Glu Ile Ile Lys Asp Ser Tyr Pro Val Asp Lys
 1795 1800 1805
 Ser Lys Leu Asp Ser Gln Lys Ala Tyr Ile Gln Ile Thr Tyr Val Glu
 1810 1815 1820

Pro Tyr Phe Asp Thr Tyr Glu Leu Lys Asp Arg Val Thr Tyr Phe Asp
 1825 1830 1835 1840
 Arg Asn Tyr Gly Leu Arg Thr Phe Leu Phe Cys Thr Pro Phe Thr Pro
 1845 1850 1855
 Asp Gly Arg Ala His Gly Glu Leu Pro Glu Gln His Lys Arg Lys Thr
 1860 1865 1870
 Leu Leu Ser Thr Asp His Ala Phe Pro Tyr Ile Lys Thr Arg Ile Arg
 1875 1880 1885
 Val Cys His Arg Glu Glu Thr Val Leu Thr Pro Val Glu Val Ala Ile
 1890 1895 1900
 Glu Asp Met Gln Lys Lys Thr Arg Glu Leu Ala Phe Ala Thr Glu Gln
 1905 1910 1915 1920
 Asp Pro Pro Asp Ala Lys Met Leu Gln Met Val Leu Gln Gly Ser Val
 1925 1930 1935
 Gly Pro Thr Val Asn Gln Gly Pro Leu Glu Val Ala Gln Val Phe Leu
 1940 1945 1950
 Ala Glu Ile Pro Glu Asp Pro Lys Leu Phe Arg His His Asn Lys Leu
 1955 1960 1965
 Arg Leu Cys Phe Lys Asp Phe Cys Lys Lys Cys Glu Asp Ala Leu Arg
 1970 1975 1980
 Lys Asn Lys Ala Leu Ile Gly Pro Asp Gln Lys Glu Tyr His Arg Glu
 1985 1990 1995 2000
 Leu Glu Arg Asn Tyr Cys Arg Leu Arg Glu Ala Leu Gln Pro Leu Leu
 2005 2010 2015
 Thr Gln Arg Leu Pro Gln Leu Met Ala Pro Thr Pro Pro Gly Leu Arg
 2020 2025 2030
 Asn Ser Leu Asn Arg Ala Ser Phe Arg Lys Ala Asp Leu
 2035 2040 2045

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<220>
 <223> human CLASP-1

<400> 110
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 Phe Ser Ser Gln Glu Lys Pro Arg Leu Leu Glu Pro Leu Asp Tyr Glu
 35 40 45

Thr Val Ile Glu Glu Leu Glu Lys Thr Tyr Arg Asn Asp Pro Leu Gln
 50 55 60
 Asp Leu Leu Phe Phe Pro Ser Asp Asp Phe Ser Ala Ala Thr Val Ser
 65 70 75 80
 Trp Asp Ile Arg Thr Leu Tyr Ser Thr Val Pro Glu Asp Ala Glu His
 85 90 95
 Lys Ala Glu Asn Leu Leu Val Lys Glu Ala Cys Lys Phe Tyr Ser Ser
 100 105 110
 Gln Trp His Val Val Asn Tyr Lys Tyr Glu Gln Tyr Ser Gly Asp Ile
 115 120 125
 Arg Gln Leu Pro Arg Ala Glu Tyr Lys Pro Glu Lys Leu Pro Ser His
 130 135 140
 Ser Phe Glu Ile Asp His Glu Asp Ala Asp Lys Asp Glu Asp Thr Thr
 145 150 155 160
 Ser His Ser Ser Ser Lys Gly Gly Gly Gly Ala Gly Gly Thr Gly Val
 165 170 175
 Phe Lys Ser Gly Trp Leu Tyr Lys Gly Asn Phe Asn Ser Thr Val Asn
 180 185 190
 Asn Thr Val Thr Val Arg Ser Phe Lys Lys Arg Tyr Phe Gln Leu Thr
 195 200 205
 Gln Leu Pro Asp Asn Ser Tyr Ile Met Asn Phe Tyr Lys Asp Glu Lys
 210 215 220
 Ile Ser Lys Glu Pro Lys Gly Cys Ile Phe Leu Asp Ser Cys Thr Gly
 225 230 235 240
 Val Val Gln Asn Asn Arg Leu Arg Lys Tyr Ala Phe Glu Leu Lys Met
 245 250 255
 Asn Asp Leu Thr Tyr Phe Val Leu Ala Ala Glu Thr Glu Ser Asp Met
 260 265 270
 Asp Glu Trp Ile His Thr Leu Asn Arg Ile Leu Gln Ile Ser Pro Glu
 275 280 285
 Gly Pro Leu Gln Gly Arg Arg Ser Thr Glu Leu Thr Asp Leu Gly Leu
 290 295 300
 Asp Ser Leu Asp Asn Ser Val Thr Cys Glu Cys Thr Pro Glu Glu Thr
 305 310 315 320
 Asp Ser Ser Glu Asn Asn Leu His Ala Asp Phe Ala Lys Tyr Leu Thr
 325 330 335
 Glu Thr Glu Asp Thr Val Lys Thr Thr Arg Asn Met Glu Arg Leu Asn
 340 345 350
 Leu Phe Ser Leu Asp Pro Asp Ile Asp Thr Leu Lys Leu Gln Lys Lys
 355 360 365

Asp Leu Leu Glu Pro Glu Ser Val Ile Lys Pro Phe Glu Glu Lys Ala
 370 375 380
 Ala Lys Arg Ile Met Ile Ile Cys Lys Ala Leu Asn Ser Asn Leu Gln
 385 390 395 400
 Gly Cys Val Thr Glu Asn Glu Asn Asp Pro Ile Thr Asn Ile Glu Pro
 405 410 415
 Phe Phe Val Ser Val Ala Leu Tyr Asp Leu Arg Asp Ser Arg Lys Ile
 420 425 430
 Ser Ala Asp Phe His Val Asp Leu Asn His Ala Ala Val Arg Gln Met
 435 440 445
 Leu Leu Gly Ala Ser Val Ala Leu Glu Asn Gly Asn Ile Asp Thr Ile
 450 455 460
 Thr Pro Arg Gln Ser Glu Glu Pro His Ile Lys Gly Leu Pro Glu Glu
 465 470 475 480
 Trp Leu Lys Phe Pro Lys Gln Ala Val Phe Ser Val Ser Asn Pro His
 485 490 495
 Ser Glu Ile Val Leu Val Ala Lys Ile Glu Lys Val Leu Met Gly Asn
 500 505 510
 Ile Ala Ser Gly Ala Glu Pro Tyr Ile Lys Asn Pro Asp Ser Asn Lys
 515 520 525
 Tyr Ala Gln Lys Ile Leu Lys Ser Asn Arg Gln Phe Cys Ser Lys Leu
 530 535 540
 Gly Lys Tyr Arg Arg Ala Phe Ala Trp Ala Val Arg Ser Val Phe Lys
 545 550 555 560
 Asp Asn Gln Gly Asn Val Asp Arg Asp Ser Arg Phe Ser Pro Leu Phe
 565 570 575
 Arg Gln Glu Ser Ser Lys Ile Ser Thr Glu Asp Leu Val Lys Leu Val
 580 585 590
 Ser Asp Tyr Arg Arg Ala Asp Arg Ile Ser Lys Met Gln Thr Ile Pro
 595 600 605
 Gly Ser Leu Asp Ile Ala Val Asp Asn Val Pro Leu Glu His Pro Asn
 610 615 620
 Cys Val Thr Ser Ser Phe Ile Pro Val Lys Pro Phe Asn Met Met Ala
 625 630 635 640
 Gln Thr Glu Pro Thr Val Glu Val Glu Glu Phe Val Tyr Asp Ser Thr
 645 650 655
 Lys Tyr Cys Arg Pro Tyr Arg Val Tyr Lys Asn Gln Ile Tyr Ile Tyr
 660 665 670
 Pro Lys His Leu Lys Tyr Asp Ser Gln Lys Cys Phe Asn Lys Ala Arg
 675 680 685

Asn Ile Thr Val Cys Ile Glu Phe Lys Asn Ser Asp Glu Glu Ser Ala
 690 695 700
 Lys Pro Leu Lys Cys Ile Tyr Gly Lys Pro Glu Gly Pro Leu Phe Thr
 705 710 715 720
 Ser Ala Ala Tyr Thr Ala Val Leu His His Ser Gln Asn Pro Asp Phe
 725 730 735
 Ser Asp Glu Val Lys Ile Glu Leu Pro Thr Gln Leu His Glu Lys His
 740 745 750
 His Ile Leu Phe Ser Phe Tyr His Val Thr Cys Asp Ile Asn Ala Lys
 755 760 765
 Ala Asn Ala Lys Lys Lys Glu Ala Leu Glu Thr Ser Val Gly Tyr Ala
 770 775 780
 Trp Leu Pro Leu Met Lys His Asp Gln Ile Ala Ser Gln Glu Tyr Asn
 785 790 795 800
 Ile Pro Ile Ala Thr Ser Leu Pro Pro Asn Tyr Leu Ser Phe Gln Asp
 805 810 815
 Ser Ala Ser Gly Lys His Gly Gly Ser Asp Ile Lys Trp Val Asp Gly
 820 825 830
 Gly Lys Pro Leu Phe Lys Val Ser Thr Phe Val Val Ser Thr Val Asn
 835 840 845
 Thr Gln Asp Pro His Val Asn Ala Phe Phe Gln Glu Cys Gln Lys Arg
 850 855 860
 Glu Lys Asp Met Ser Gln Ser Pro Thr Ser Asn Phe Ile Arg Ser Cys
 865 870 875 880
 Lys Asn Leu Leu Asn Val Glu Lys Ile His Ala Ile Met Ser Phe Leu
 885 890 895
 Pro Ile Ile Leu Asn Gln Leu Phe Lys Val Leu Val Gln Asn Glu Glu
 900 905 910
 Asp Glu Ile Thr Thr Thr Val Thr Arg Val Leu Pro Asp Ile Val Ala
 915 920 925
 Lys Cys His Glu Glu Gln Leu Asp His Ser Val Gln Ser Tyr Ile Lys
 930 935 940
 Phe Val Phe Lys Thr Arg Ala Cys Lys Glu Arg Pro Val His Glu Asp
 945 950 955 960
 Leu Ala Lys Asn Val Thr Gly Leu Leu Lys Ser Asn Asp Ser Pro Thr
 965 970 975
 Val Lys His Val Leu Lys His Ser Trp Phe Phe Phe Ala Ile Ile Leu
 980 985 990
 Lys Ser Met Ala Gln His Leu Ile Asp Thr Asn Lys Ile Gln Leu Pro
 995 1000 1005

Arg Pro Gln Arg Phe Pro Glu Ser Tyr Gln Asn Glu Leu Asp Asn Leu
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 Val Met Val Leu Ser Asp His Val Ile Trp Lys Tyr Lys Asp Ala Leu
 1025 1030 1035 1040
 Glu Glu Thr Arg Arg Ala Thr His Ser Val Ala Arg Phe Leu Lys Arg
 1045 1050 1055
 Cys Phe Thr Phe Met Asp Arg Gly Cys Val Phe Lys Met Val Asn Asn
 1060 1065 1070
 Tyr Ile Ser Met Phe Ser Ser Gly Asp Leu Lys Thr Leu Cys Gln Tyr
 1075 1080 1085
 Lys Phe Asp Phe Leu Gln Glu Val Cys Gln His Glu His Phe Ile Pro
 1090 1095 1100
 Leu Cys Leu Pro Ile Arg Ser Ala Asn Ile Pro Asp Pro Leu Thr Pro
 1105 1110 1115 1120
 Ser Glu Ser Thr Gln Glu Leu His Ala Ser Asp Met Pro Glu Tyr Ser
 1125 1130 1135
 Val Thr Asn Glu Phe Cys Arg Lys His Phe Leu Ile Gly Ile Leu Leu
 1140 1145 1150
 Arg Glu Val Gly Phe Ala Leu Gln Glu Asp Gln Asp Val Arg His Leu
 1155 1160 1165
 Ala Leu Ala Val Leu Lys Asn Leu Met Ala Lys His Ser Phe Asp Asp
 1170 1175 1180
 Arg Tyr Arg Glu Pro Arg Lys Gln Ala Gln Ile Ala Ser Leu Tyr Met
 1185 1190 1195 1200
 Pro Leu Tyr Gly Met Leu Leu Asp Asn Met Pro Arg Ile Tyr Leu Lys
 1205 1210 1215
 Asp Leu Tyr Pro Phe Thr Val Asn Thr Ser Asn Gln Gly Ser Arg Asp
 1220 1225 1230
 Asp Leu Ser Thr Asn Gly Gly Phe Gln Ser Gln Thr Ala Ile Lys His
 1235 1240 1245
 Ala Asn Ser Val Asp Thr Ser Phe Ser Lys Asp Val Leu Asn Ser Ile
 1250 1255 1260
 Ala Ala Phe Ser Ser Ile Ala Ile Ser Thr Val Asn His Ala Asp Ser
 1265 1270 1275 1280
 Arg Ala Ser Leu Ala Ser Leu Asp Ser Asn Pro Ser Thr Asn Glu Lys
 1285 1290 1295
 Ser Ser Glu Lys Thr Asp Asn Cys Glu Lys Ile Pro Arg Pro Leu Ala
 1300 1305 1310
 Leu Ile Gly Ser Thr Leu Arg Phe Asp Arg Leu Asp Gln Ala Glu Thr
 1315 1320 1325

Arg Ser Leu Leu Met Cys Phe Leu His Ile Met Lys Thr Ile Ser Tyr
 1330 1335 1340
 Glu Thr Leu Ile Ala Tyr Trp Gln Arg Ala Pro Ser Pro Glu Val Ser
 1345 1350 1355 1360
 Asp Phe Phe Ser Ile Leu Asp Val Cys Leu Gln Asn Phe Arg Tyr Leu
 1365 1370 1375
 Gly Lys Arg Asn Ile Ile Arg Lys Ile Ala Ala Ala Phe Lys Phe Val
 1380 1385 1390
 Gln Ser Thr Gln Asn Asn Gly Thr Leu Lys Gly Ser Asn Pro Ser Cys
 1395 1400 1405
 Gln Thr Ser Gly Leu Leu Ala Gln Trp Met His Ser Thr Ser Arg His
 1410 1415 1420
 Glu Gly His Lys Gln His Arg Ser Gln Thr Leu Pro Ile Ile Arg Gly
 1425 1430 1435 1440
 Lys Asn Ala Leu Ser Asn Pro Lys Leu Leu Gln Met Leu Asp Asn Thr
 1445 1450 1455
 Met Thr Ser Asn Ser Asn Glu Ile Asp Ile Val His His Val Asp Thr
 1460 1465 1470
 Glu Ala Asn Ile Ala Thr Glu Gly Cys Leu Thr Ile Leu Asp Leu Val
 1475 1480 1485
 Ser Leu Phe Thr Gln Thr His Gln Arg Gln Leu Gln Gln Cys Asp Cys
 1490 1495 1500
 Gln Asn Ser Leu Met Lys Arg Gly Phe Asp Thr Tyr Met Leu Phe Phe
 1505 1510 1515 1520
 Gln Val Asn Gln Ser Ala Thr Ala Leu Lys His Val Phe Ala Ser Leu
 1525 1530 1535
 Arg Leu Phe Val Cys Lys Phe Pro Ser Ala Phe Phe Gln Gly Pro Ala
 1540 1545 1550
 Asp Leu Cys Gly Ser Phe Cys Tyr Glu Val Leu Lys Cys Cys Asn His
 1555 1560 1565
 Arg Ser Arg Ser Thr Gln Thr Glu Ala Ser Ala Leu Leu Tyr Leu Phe
 1570 1575 1580
 Met Arg Lys Asn Phe Glu Phe Asn Lys Gln Lys Ser Ile Val Arg Ser
 1585 1590 1595 1600
 His Leu Gln Leu Ile Lys Ala Val Ser Gln Leu Ile Ala Asp Ala Gly
 1605 1610 1615
 Ile Gly Gly Ser Arg Phe Gln His Ser Leu Ala Ile Thr Asn Asn Phe
 1620 1625 1630
 Ala Asn Gly Asp Lys Gln Met Lys Asn Ser Asn Phe Pro Ala Glu Val
 1635 1640 1645

Lys Asp Leu Thr Lys Arg Ile Arg Thr Val Leu Met Ala Thr Ala Gln
 1650 1655 1660
 Met Lys Glu His Glu Lys Asp Pro Glu Met Leu Val Asp Leu Gln Tyr
 1665 1670 1675 1680
 Ser Leu Ala Asn Ser Tyr Ala Ser Thr Pro Glu Leu Arg Arg Thr Trp
 1685 1690 1695
 Leu Glu Ser Met Ala Lys Ile His Ala Arg Asn Gly Asp Leu Ser Glu
 1700 1705 1710
 Ala Ala Met Cys Tyr Ile His Ile Ala Ala Leu Ile Ala Glu Tyr Leu
 1715 1720 1725
 Lys Arg Lys Gly Tyr Trp Lys Val Glu Lys Ile Cys Thr Ala Ser Leu
 1730 1735 1740
 Leu Ser Glu Asp Thr His Pro Cys Asp Ser Asn Ser Leu Leu Thr Thr
 1745 1750 1755 1760
 Pro Ser Gly Gly Ser Met Phe Ser Met Gly Trp Pro Ala Phe Leu Ser
 1765 1770 1775
 Ile Thr Pro Asn Ile Lys Glu Glu Gly Ala Ala Lys Glu Asp Ser Gly
 1780 1785 1790
 Met His Asp Thr Pro Tyr Asn Glu Asn Ile Leu Val Glu Gln Leu Tyr
 1795 1800 1805
 Met Cys Gly Glu Phe Leu Trp Lys Ser Glu Arg Tyr Glu Leu Ile Ala
 1810 1815 1820
 Asp Val Asn Lys Pro Ile Ile Ala Val Phe Glu Lys Gln Arg Asp Phe
 1825 1830 1835 1840
 Lys Lys Leu Ser Asp Leu Tyr Tyr Asp Ile His Arg Ser Tyr Leu Lys
 1845 1850 1855
 Val Ala Glu Val Val Asn Ser Glu Lys Arg Leu Phe Gly Arg Tyr Tyr
 1860 1865 1870
 Arg Val Ala Phe Tyr Gly Gln Gly Phe Phe Glu Glu Glu Glu Gly Lys
 1875 1880 1885
 Glu Tyr Ile Tyr Lys Glu Pro Lys Leu Thr Gly Leu Ser Glu Ile Ser
 1890 1895 1900
 Gln Arg Leu Leu Lys Leu Tyr Ala Asp Lys Phe Gly Ala Asp Asn Val
 1905 1910 1915 1920
 Lys Ile Ile Gln Asp Ser Asn Lys Val Asn Pro Lys Asp Leu Asp Pro
 1925 1930 1935
 Lys Tyr Ala Tyr Ile Gln Val Thr Tyr Val Thr Pro Phe Phe Glu Glu
 1940 1945 1950
 Lys Glu Ile Glu Asp Arg Lys Thr Asp Phe Glu Met His His Asn Ile
 1955 1960 1965

Asn Arg Phe Val Phe Glu Thr Pro Phe Thr Leu Ser Gly Lys Lys His
 1970 1975 1980
 Gly Gly Val Ala Glu Gln Cys Lys Arg Arg Thr Ile Leu Thr Thr Ser
 1985 1990 1995 2000
 His Leu Phe Pro Tyr Val Lys Lys Arg Ile Gln Val Ile Ser Gln Ser
 2005 2010 2015
 Ser Thr Glu Leu Asn Pro Ile Glu Val Ala Ile Asp Glu Met Ser Arg
 2020 2025 2030
 Lys Val Ser Glu Leu Asn Gln Leu Cys Thr Met Glu Glu Val Asp Met
 2035 2040 2045
 Ile Ser Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Lys Val Asn
 2050 2055 2060
 Ala Gly Pro Met Ala Tyr Ala Arg Ala Phe Leu Glu Glu Thr Asn Ala
 2065 2070 2075 2080
 Lys Lys Tyr Pro Asp Asn Gln Val Lys Leu Leu Lys Glu Ile Phe Arg
 2085 2090 2095
 Gln Phe Ala Asp Ala Cys Gly Gln Ala Leu Asp Val Asn Glu Arg Leu
 2100 2105 2110
 Ile Lys Glu Asp Gln Leu Glu Tyr Gln Glu Glu Leu Arg Ser His Tyr
 2115 2120 2125
 Lys Asp Met Leu Ser Glu Leu Ser Thr Val Met Asn Glu Gln Ile Thr
 2130 2135 2140
 Gly Arg Asp Asp Leu Ser Lys Arg Gly Val Asp Gln Thr Cys Thr Arg
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 oligonucleotide C7AS16

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